

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

- * Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
- * Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 21:59:17 ; Search time 93.6 Seconds
(without alignments)
107.136 Million cell updates/sec

Title: US-10-751-235-10
Perfect score: 122
Sequence: 1 LVAEVSEFLFGSGFAIARGPLWTA 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	24	5	US-10-751-235-10
2	122	100.0	222	4	US-10-424-599-265810
3	122	100.0	539	5	US-10-751-235-4
4	122	100.0	560	5	US-10-739-930-6317
5	114	93.4	208	5	US-10-751-235-21
6	110	90.2	362	5	US-10-751-235-18
7	110	90.2	382	4	US-10-425-114-70634
8	110	90.2	531	4	US-10-437-963-117686
9	110	90.2	545	5	US-10-751-235-17
10	110	90.2	561	5	US-10-751-235-16
11	110	90.2	588	5	US-10-751-235-52
12	110	90.2	624	4	US-10-425-115-332853
13	59	48.4	167	4	US-10-282-122A-52949
14	59	48.4	342	4	US-10-282-122A-52999
15	58	47.5	501	4	US-10-425-115-244178
16	58	47.5	588	4	US-10-437-963-139807
17	58	47.5	632	5	US-10-751-235-34
18	58	47.5	662	4	US-10-425-114-38827
19	57	46.7	342	5	US-10-751-235-37
20	57	46.7	508	5	US-10-751-235-35
21	56	45.9	344	4	US-10-369-493-17393
22	54	44.3	579	5	US-10-751-235-38
23	54	44.3	595	5	US-10-751-235-33
24	52.5	43.0	97	3	US-09-738-626-4993
25	51	41.8	1709	4	US-10-156-761-11180
26	50	41.0	212	4	US-10-424-599-195097
27	50	41.0	350	4	US-10-282-122A-60963

28	49.5	40.6	287	4	US-10-369-493-17225	Sequence 17225, A
29	49	40.2	148	4	US-10-424-599-223289	Sequence 223289, A
30	49	40.2	360	4	US-10-369-493-7853	Sequence 7853, Ap
31	49	40.2	572	4	US-10-167-994-2	Sequence 2, Appli
32	49	40.2	572	4	US-10-017-479-2	Sequence 2, Appli
33	49	40.2	572	5	US-10-718-359-2	Sequence 2, Appli
34	49	40.2	572	6	US-11-097-143-7737	Sequence 7737, Ap
35	49	40.2	572	6	US-11-097-143-27501	Sequence 27501, A
36	48	39.3	107	4	US-10-424-599-273682	Sequence 273682, A
37	48	39.3	113	4	US-10-425-115-305171	Sequence 305171, A
38	48	39.3	173	4	US-10-369-493-48087	Sequence 48087, A
39	48	39.3	303	4	US-10-369-493-10381	Sequence 10381, A
40	48	39.3	394	4	US-10-425-114-45724	Sequence 45724, A
41	48	39.3	431	4	US-10-424-599-273679	Sequence 273679, A
42	48	39.3	523	4	US-10-230-026-30	Sequence 30, Appl
43	48	39.3	523	5	US-10-486-307-30	Sequence 30, Appl
44	48	39.3	703	4	US-10-437-963-172007	Sequence 172007, A
45	48	39.3	1032	4	US-10-389-566-1449	Sequence 1449, Ap

ALIGNMENTS

RESULT 1
US-10-751-235-10
; Sequence 10, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: DellaPenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 10
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-751-235-10

Query Match 100.0%; Score 122; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.1e-12; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 1 LVAEVSEFLFGSGFAIARGPLWTA 24
|||||
DB 1 LVAEVSEFLFGSGFAIARGPLWTA 24
|||||

RESULT 2
US-10-424-599-265810
; Sequence 265810, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 265810
; LENGTH: 222
; TYPE: PRT

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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_82046C.1.pap
US-10-424-599-265810

Query Match      100.0%; Score 122; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVAEVSEFLFGSGFAIAEGPLWTA 24
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Db 157 LVAEVSEFLFGSGFAIAEGPLWTA 180

RESULT 3
US-10-751-235-4
; Sequence 4, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: DellaPenna, Dean
; APPLICANT: Tian, Li
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-751-235-4

Query Match      100.0%; Score 122; DB 5; Length 539;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVAEVSEFLFGSGFAIAEGPLWTA 24
    |||||
Db 144 LVAEVSEFLFGSGFAIAEGPLWTA 167

RESULT 4
US-10-739-930-6317
; Sequence 6317, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6317
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; OTHER INFORMATION: Clone ID: ARATH-23APR03-C3001_1.p
US-10-739-930-6317

Query Match      100.0%; Score 122; DB 5; Length 560;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVAEVSEFLFGSGFAIAEGPLWTA 24
    |||||
Db 165 LVAEVSEFLFGSGFAIAEGPLWTA 188

RESULT 5
US-10-751-235-21
; Sequence 21, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: DellaPenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Helianthus annuus
US-10-751-235-21

Query Match      93.4%; Score 114; DB 5; Length 208;
Best Local Similarity 95.8%; Pred. No. 6.6e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LVAEVSEFLFGSGFAIAEGPLWTA 24
    |||||
Db 29 LVAEVSEFLFGSGFAIAEGSLWTA 52

RESULT 6
US-10-751-235-18
; Sequence 18, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: DellaPenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-751-235-18

Query Match      90.2%; Score 110; DB 5; Length 362;
Best Local Similarity 95.7%; Pred. No. 5.4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LVAEVSEFLFGSGFAIAEGPLWT 23
    |||||
Db 141 LVAEVSEFLFGSGFAIAEGALWT 163

RESULT 7
US-10-425-114-70634
; Sequence 70634, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70634
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMOL7009E12_FLI.pep
US-10-425-114-70634

Query Match 90.2%; Score 110; DB 4; Length 382;
Best Local Similarity 95.7%; Pred. No. 5.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAEGPLWT 23
|||||
Db 109 LVAEVSEFLFGSGFAIAEGDLWT 131
|||||

RESULT 8
US-10-437-963-117686
; Sequence 117686, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 117686
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_21069C.1.pep
US-10-437-963-117686

Query Match 90.2%; Score 110; DB 4; Length 531;
Best Local Similarity 95.7%; Pred. No. 8.3e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAEGPLWT 23
|||||
Db 152 LVAEVSEFLFGSGFAIAEGALWT 174
|||||

RESULT 9
US-10-751-235-17
; Sequence 17, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: Dellapenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17

; LENGTH: 545
; TYPE: PRT
; ORGANISM: Hordeum vulgare
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (529)-(529)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-751-235-17

Query Match 90.2%; Score 110; DB 5; Length 545;
Best Local Similarity 95.7%; Pred. No. 8.5e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAEGPLWT 23
|||||
Db 136 LVAEVSEFLFGSGFAIAEGALWT 158
|||||

RESULT 10
US-10-751-235-16
; Sequence 16, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: Dellapenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-751-235-16

Query Match 90.2%; Score 110; DB 5; Length 561;
Best Local Similarity 95.7%; Pred. No. 8.8e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAEGPLWT 23
|||||
Db 152 LVAEVSEFLFGSGFAIAEGALWT 174
|||||

RESULT 11
US-10-751-235-52
; Sequence 52, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: Dellapenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-751-235-52

Query Match 90.2%; Score 110; DB 5; Length 588;
Best Local Similarity 95.7%; Pred. No. 9.3e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSFLFGSGFAIAEGPLWT 23
Db 154 LVAEVSFLFGSGFAIAEGALWT 176

RESULT 12

US-10-425-115-332853
; Sequence 332853, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 332853
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(624)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_66678C.1.pep
US-10-425-115-332853

Query Match 90.2%; Score 110; DB 4; Length 624;
Best Local Similarity 95.7%; Pred. No. 9.9e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSFLFGSGFAIAEGPLWT 23
Db 193 LVAEVSFLFGSGFAIAEGDLWT 215

RESULT 13

US-10-282-122A-52949
; Sequence 52949, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52949
; LENGTH: 342

; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52949
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-52949

Query Match 48.4%; Score 59; DB 4; Length 167;
Best Local Similarity 50.0%; Pred. No. 0.36;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVAEVSFLFGSGFAIAEGP 20
Db 113 IIDEVTDIFIGMGSIAEGP 132

RESULT 14

US-10-282-122A-52999
; Sequence 52999, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52999
; LENGTH: 342

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; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-52999

Query Match      48.4%; Score 59; DB 4; Length 342;
Best Local Similarity 50.0%; Pred. No. 0.8;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy      1 LVAEVSEFLFGSGFAIAEGP 20
Db      116 IIDVTDIFIGMFGSIAEGP 135

RESULT 15
US-10-425-115-244178
; Sequence 244178, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 244178
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_154276C.1.pep
US-10-425-115-244178

Query Match      47.5%; Score 58; DB 4; Length 501;
Best Local Similarity 40.9%; Pred. No. 1.8;
Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy      1 LVAEVSEFLFGSGFAIAEGPLW 22
Db      64 ILAEILEFVMTGLIPADGEIW 85

Search completed: March 7, 2006, 22:04:14
Job time : 94.6 secs
```

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 21:43:03 ; Search time 352.2 Seconds
(without alignments)
44.911 Million cell updates/sec

Title: US-10-751-235-11

Perfect score: 177

Sequence: 1 MESSLPSPSSSYSLFTAKPRLLSPKPKFTFSIR 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseq1990s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	177	100.0	36	9 AEB16913	Aebi6913 Thale cre
2	177	100.0	539	9 AEB16908	Aebi6908 Thale cre
3	177	100.0	560	8 ADT56240	Adt56240 Plant pol
4	75.5	42.7	386	3 AAY44631	Aay44631 A. thalia
5	75.5	42.7	386	4 AAB85456	Aab85456 Arabidops
6	63	35.6	260	8 ADM48270	Adm48270 Polytype
7	62.5	35.3	2016	4 ABB63911	Abb63911 Drosophil
8	60	33.9	222	3 AAG26703	Aag26703 Arabidops
9	60	33.9	355	5 ABB93995	Abb93995 Herbicida
10	60	33.9	389	3 AAG54022	Aag54022 Arabidops
11	60	33.9	389	3 AAG22506	Aag22506 Arabidops
12	59.5	33.6	317	3 AAG59958	Aag59958 Arabidops
13	59.5	33.6	317	3 AAG10212	Aag10212 Arabidops
14	59.5	33.6	319	3 AAG10211	Aag10211 Arabidops
15	59.5	33.6	319	3 AAG59957	Aag59957 Arabidops
16	59.5	33.6	319	5 ABB93989	Abb93989 Herbicida
17	59.5	33.6	319	8 ADT55654	Adt55654 Plant pol
18	59	33.3	1545	4 ABB65577	Abb65577 Drosophil
19	57	32.2	100	3 AAG43792	Aag43792 Arabidops
20	56	31.6	48	4 ABBG04863	AbbG04863 Novel hum
21	56	31.6	407	3 AAG22122	Aag22122 Arabidops
22	56	31.6	434	3 AAG22121	Aag22121 Arabidops
23	56	31.6	474	8 ADN74381	Adn74381 Thale cre
24	56	31.6	883	4 ABBG2230	AbbG2230 Drosophil

25 55.5 31.4 370 8 ADX66893 Axi66893 Plant ful
26 55 31.1 137 3 AAG17405 Aag17405 Arabidops
27 55 31.1 143 3 AAG17404 Aag17404 Arabidops
28 54.5 30.8 92 3 AAG16401 Aag16401 Arabidops
29 54.5 30.8 121 3 AAG16400 Aag16400 Arabidops
30 54.5 30.8 416 8 ADI42851 Adi42851 Plant tra
31 54.5 30.8 416 8 ADO03046 ADO03046 Thalecres
32 54.5 30.8 898 7 ABM87814 Abm87814 Rice abio
33 54.5 30.8 2027 4 AAE10987 Aae10987 Mouse pre
34 54 30.5 205 5 ABB79956 Abb79956 Arabidops
35 54 30.5 205 6 ABR40828 Abr40828 Arabidops
36 54 30.5 251 8 ADT60146 Adt60146 Plant pol
37 54 30.5 271 7 ABM86366 Abm86366 Rice abio
38 54 30.5 307 4 ABG22889 Abg22889 Novel hum
39 54 30.5 403 3 AAG53830 Aag53830 Arabidops
40 54 30.5 403 3 AAG16661 Aag16661 Arabidops
41 54 30.5 430 5 AAU93039 Aau93039 Arabidops
42 54 30.5 430 5 ABB79954 Abb79954 Arabidops
43 54 30.5 430 5 ABB79955 Abb79955 Arabidops
44 54 30.5 430 7 ADB31801 Adb31801 Plant (A.
45 54 30.5 430 7 ADC46705 Adc46705 Thalecres

ALIGNMENTS

RESULT 1

AEB16913

ID AEB16913 standard; peptide; 36 AA.

XX AEB16913;

DT 08-SEP-2005 (first entry)

DE Thale cress chloroplast-targeting N-terminal peptide, SEQ ID NO: 11.

XX Pigment; metabolic engineering; antioxidant; transgenic plant;

XX cytochrome P450.

OS Arabidopsis thaliana.

XX US2005150002-A1.

XX 07-JUL-2005.

XX 02-JAN-2004; 2004US-00751235.

XX 02-JAN-2004; 2004US-00751235.

XX (DELL/) DELLAPENNA D.

XX (TIAN/) TIAN L.

XX (KIM/) KIM J.

XX Dellapenna D, Tian L, Kim J;

XX WPI; 2005-487994/49.

XX New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.

XX Claim 8; SEQ ID NO 11; 135pp; English.

XX The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epiallon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is thale cress chlorophyll-targeting N-terminal transit peptide.

XX

SQ Sequence 36 AA;
 Query Match 100.0%; Score 177; DB 9; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSLFPSSSSVSLFTAKPTLLSPKPKFTFSIR 36
 |||||
 DB 1 MESSLFPSSSSVSLFTAKPTLLSPKPKFTFSIR 36
 |||||

RESULT 2
 AEB16908
 ID AEB16908 standard; protein; 539 AA.
 AC AEB16908;
 XX 08-SEP-2005 (first entry)
 DT Thale cress LUT1 (cytochrome P450 97C1) protein, SEQ ID NO: 4.
 DE Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C1;
 KW cytochrome P450 97C1.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX Key Location/Qualifiers
 XX Region 1..36
 FT /note= "Chloroplast-targeting N-terminal transit peptide"
 FT /note= "Encoded by bases of positions 496 to 650"
 FT Misc-difference 166..167
 FT /note= "Encoded by bases of positions 942 to 1037"
 FT Misc-difference 265..266
 FT /note= "Encoded by bases of positions 1242 to 1326"
 FT Misc-difference 332..333
 FT /note= "Molecular oxygen binding pocket"
 FT Region 347..352
 FT /note= "Encoded by bases of positions 1420 to 1523"
 FT Misc-difference 365..366
 FT /note= "Encoded by bases of positions 1662 to 1841"
 FT Misc-difference 413..414
 FT /note= "Encoded by bases of positions 1839 to 12005"
 FT Misc-difference 449..450
 FT /note= "Encoded by bases of positions 2081 to 2183"
 FT Misc-difference 476..477
 FT /note= "Cysteine motif region"
 FT Region 480..489
 FT /note= "Encoded by bases of positions 2340 to 2440"
 FT Misc-difference 530..531
 FT /note= "Encoded by bases of positions 2340 to 2440"
 XX US2005150002-A1.
 XX 07-JUL-2005.
 XX 02-JAN-2004; 2004US-00751235.
 XX 02-JAN-2004; 2004US-00751235.
 XX (DELL/) DELLAPENNA D.
 XX (TIAN/) TIAN L.
 XX (KIMJ/) KIM J.
 XX Dellapenna D, Tian L, Kim J;
 XX WPI; 2005-487984/49.
 XX New expression vector comprising a nucleic acid sequence encoding a
 PT polypeptide having monooxygenase P450 activity, useful in altering the
 PT carotenoid production in a plant for enhancing production of specific
 PT carotenoid compounds.
 XX Claim 9; SEQ ID NO 4; 135pp; English.

CC The present invention relates to genes, proteins and methods comprising
 CC carotenoid monooxygenases in the cytochrome P450 family. The invention
 CC also relates to altering carotenoid ratios in plants and microorganisms
 CC using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The
 CC invention is useful in altering the carotenoid production in a plant for
 CC enhancing production of specific carotenoid compounds that are potent
 CC antioxidants. The present sequence is thale cress LUT1 (cytochrome P450
 CC monooxygenase (CYP97C1); At3g53130 gene) protein. Note: The current
 CC sequence is that of thale cress LUT1 protein that is encoded by cDNA
 CC located on chromosome 3.
 XX
 SQ Sequence 539 AA;
 Query Match 100.0%; Score 177; DB 9; Length 539;
 Best Local Similarity 100.0%; Pred. No. 4.5e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSLFPSSSSVSLFTAKPTLLSPKPKFTFSIR 36
 |||||
 DB 1 MESSLFPSSSSVSLFTAKPTLLSPKPKFTFSIR 36
 |||||

RESULT 3
 ADT56240
 ID ADT56240 standard; protein; 560 AA.
 AC ADT56240;
 XX 13-JAN-2005 (first entry)
 DT Plant polypeptide, SEQ ID 6317.
 DE Plant; transgenic; cold tolerance; growth rate; drought tolerance;
 KW disease resistance; galactomannan production; plant growth regulator;
 KW heat tolerance; herbicide tolerance; lignin production;
 KW extreme osmotic condition tolerance; pathogens resistance;
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.
 XX Viridiplantae.
 OS US2004216190-A1.
 XX 28-OCT-2004.
 XX 18-DEC-2003; 2003US-00739930.
 XX 28-APR-2003; 2003US-00424599.
 XX 28-APR-2003; 2003US-00425115.
 XX (KOVA/) KOVALIC D K.
 XX Kovalic DK;
 XX WPI; 2004-757369/74.
 XX New recombinant DNA constructs useful in the field of biochemistry and
 PT Genetics, and in particular for producing transgenic plants with improved
 PT biological characteristics.
 XX Claim 2; SEQ ID NO 6317; 14pp; English.
 XX The invention relates a recombinant DNA construct comprising a
 CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
 CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
 CC Arabidopsis, wheat and rape but the specification does not indicate which
 CC sequences is derived from which organism. Also included is a method of
 CC producing a plant having an improved property, comprising transforming a
 CC plant with a recombinant DNA construct comprising a promoter region
 CC functional in a plant cell operably joined to a polynucleotide encoding a
 CC polypeptide associated with the property, and growing the transformed
 CC plant. The property is selected from improving plant cold tolerance, for
 CC manipulating growth rate in plant cells by modification of the cell cycle

CC pathway, for improving plant drought tolerance, for providing increased
CC resistance to plant disease, for galactomannan production, for production
CC of plant growth regulators, for improving plant heat tolerance, for
CC improving plant tolerance to herbicides, for increasing the rate of
CC homologous recombination in plants, for lignin production, for improving
CC plant tolerance to extreme osmotic conditions, for improving plant
CC tolerance to pathogens or pests, for yield improvement by modification of
CC photosynthesis, for modifying seed oil yield and/or content, for
CC modifying seed protein yield and/or content, for yield improvement by
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
CC and for yield improvement by providing improved plant growth and
CC development under at least one stress condition. The polynucleotide may
CC also encode a plant transcription factor. The methods and compositions of
CC the present invention are useful in the field of biochemistry and
CC genetics, in particular for producing transgenic plants with improved
CC biological characteristics such as increased yield, improved nitrogen
CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 5544 plant protein
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX SQ Sequence 560 AA;

Query Match 100.0%; Score 177; DB 8; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.7e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSLFPSSSSSYSLFTAKPTRLSPKPKFTFSIR 36
DB 22 MESSLFPSSSSSYSLFTAKPTRLSPKPKFTFSIR 57

RESULT 4

AA44631

ID AAY44631 standard; protein; 386 AA.

AC AAY44631;

DT 07-APR-2000 (first entry)

XX A. thaliana AIR synthetase pre-protein.

XX 5'-phosphoribosyl-5-aminoimidazole synthetase; weed growth;
KW purine biosynthesis; recombinant AIR synthetase; herbicide.

XX Arabidopsis thaliana.

XX WO9967402-A2.

XX 29-DEC-1999.

XX 22-JUN-1999; 99WO-EP004309.

XX 24-JUN-1998; 98US-00103895.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Ward ER, Guyer CD, Potter SL, Subramanian V, Walters E;

XX WPI; 2000-136986/12.

DR N-PSDB; AA249679.

XX New isolated enzyme with phosphoribosyl-5-aminoimidazole synthetase
PT activity, used to screen for herbicides or to produce herbicide-tolerant
PT plants.

XX Claim 3; Page 53-54; 58pp; English.

XX

CC The present sequence is A. thaliana AIR (5'-phosphoribosyl-5-
CC aminimidazole) synthetase pre-protein, an enzyme involved in de novo
CC purine biosynthesis. The cDNA is deposited in E. coli strain DH5apasm
CC designated as NRRL accession number B-21976. Recombinantly produced AIR
CC synthetase enzyme can be used in screening chemicals for herbicidal
CC activity. Plants having modified enzyme activity are tolerant to
CC inhibition by herbicides. Herbicide-tolerant AIR synthetase is also
CC useful as a selectable marker in plants

XX SQ Sequence 386 AA;

Query Match 42.7%; Score 75.5; DB 3; Length 386;
Best Local Similarity 48.6%; Pred. No. 0.063;
Matches 17; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 1 MESSLFPSSSSSYSLFTAKPTRLSPKPKFTFSI 35
DB 1 MEARILQSSSCYSSLYTVNRGRFSPKPKP---FSV 32

RESULT 5

AAB85456

ID AAB85456 standard; protein; 386 AA.

AC AAB85456;

DT 25-SEP-2001 (first entry)

XX Arabidopsis AIR synthetase.

XX 5'-phosphoribosyl-5-aminoimidazole synthetase; AIR synthetase;

KW Arabidopsis; transgenic; herbicide; enzyme.

XX Arabidopsis thaliana.

XX US6271445-B1.

XX 07-AUG-2001.

XX 22-JUN-1999; 99US-00338420.

XX 24-JUN-1998; 98US-0155234P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Ward ER, Guyer DC, Potter SL, Subramanian V, Walters E;

XX WPI; 2001-475191/51.

DR N-PSDB; AAH23384.

XX Novel isolated nucleic acid encoding a 5'-phosphoribosyl-5-aminoimidazole
PT synthase, used to transform plant cells, for use in screening for
PT herbicides.

XX Claim 1; Col 29-32; 21pp; English.

XX The invention relates to a 5'-phosphoribosyl-5-aminoimidazole (AIR)
CC synthetase from Arabidopsis. The AIR synthetase protein can be expressed
CC by standard recombinant methodology. Nucleic acids encoding the AIR
CC synthetase are used for producing transgenic plants and plant cells, for
CC screening herbicidal compounds which inhibit the enzymatic activity of
CC AIR synthetase. The present sequence represents an Arabidopsis AIR
CC synthetase sequence

XX SQ Sequence 386 AA;

Query Match 42.7%; Score 75.5; DB 4; Length 386;
Best Local Similarity 48.6%; Pred. No. 0.063;
Matches 17; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 1 MESSLFPSSSSSYSLFTAKPTRLSPKPKFTFSI 35
||: : ||| ||||: : ||||| ||:

Db 1 MEARILQSSSCVSLYTVNRGRFSPKPK---FSV 32

RESULT 6
ADM48270
ID ADM48270 standard; protein; 260 AA.
XX
AC ADM48270;
XX
DT 03-JUN-2004 (first entry)
XX
DE Polypeptide sequence #320 useful in producing transgenic plants.
XX
KW Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
KW osmotic stress; sugar transport; cell cycle pathway; plant height;
KW carbohydrate transport; crop productivity; plant growth;
KW stress resistance; disease resistance; insect resistance; heat tolerance;
KW nitrogen assimilation; water stress tolerance;
KW photosynthetic carbon fixation; virus resistance; gene therapy.
XX
OS Glycine max.
XX
PN US2003233670-A1.
XX
PD 18-DEC-2003.
XX
PF 04-DEC-2002; 2002US-00310154.
XX
PR 04-DEC-2001; 2001US-0337358P.
XX
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
XX
PI Edgerton MD, Chomet PS, Laccetti LB;
XX
DR WPI; 2004-061374/06.
DR N-PSDB; ADM47902.
XX
PT New polynucleotide, useful for manipulating plant protein quality,
PT improving plant growth, yield and crop productivity or grain composition
PT or producing plants with improved properties.
XX
PS Claim 8; SEQ ID NO 688; 144pp; English.
XX
CC The present invention relates to polynucleotide sequences, and the
CC proteins they encode. The sequences are isolated from a variety of
CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
CC polynucleotide and polypeptide sequences of the invention are useful in
CC the production of transgenic plants that have improved properties. Also
CC disclosed are methods of producing fertile transgenic plants, preferably
CC maize, with desired phenotypes. The polynucleotide and polypeptide
CC sequences are useful for improving plants by providing protection against
CC osmotic stress, improving altering sugar transport and/or metabolism,
CC modifying the cell cycle pathway, reducing plant height, modifying
CC carbohydrate transport, improving crop productivity, improving plant
CC growth and stress resistance, improving disease resistance, improving
CC insect resistance, improving cold or heat tolerance, improving nitrogen
CC assimilation, improving stalk strength, improving water stress tolerance,
CC improving photosynthetic carbon fixation, improving biotic and abiotic
CC stress resistance, improving resistance to oxidative stress, providing
CC increased vigour, reducing senescence, and conferring virus resistance.
CC The present sequence represents a polypeptide sequence of the invention.
CC Note: The sequence data for this patent is not provided in the printed
CC specification but is obtained in electronic format from the USPTO website
CC at seqdata.uspto.gov.
XX
SQ Sequence 260 AA;

Query Match 35.6%; Score 63; DB 8; Length 260;
Best Local Similarity 46.2%; Pred. No. 2.3;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 10 SSSYSLFTAKTRLLSPKPKFTFSI 35
|::|||:|||||:
Db 4 SATSASLFSANPTPLFSPKPSLSLHL 29

RESULT 7
ABB63911
ID ABB63911 standard; protein; 2016 AA.
XX
AC ABB63911;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 18525.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL08014.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 18525; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2016 AA;

Query Match 35.3%; Score 62.5; DB 4; Length 2016;
Best Local Similarity 47.4%; Pred. No. 30;
Matches 18; Conservative 4; Mismatches 11; Indels 5; Gaps 2

Qy 3 SSSLFSSPSSSSYSLFTAKP----TRLLSPKPKFTFSI 35
|||||:|||||:|:
Db 986 SSSLFSPQVDSLSLFAFPPTSANTTILTPADTTSTL 1023

RESULT 8
AAG26703
ID AAG26703 standard; protein; 222 AA.
XX
AC AAG26703;
XX
DT 17-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 31259.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 23-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136332P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139453P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
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PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 24-JUN-1999; 99US-0140354P.
PR 28-JUN-1999; 99US-0140695P.
PR 29-JUN-1999; 99US-0140823P.
PR 30-JUN-1999; 99US-0140991P.
PR 01-JUL-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR	20-SEP-1999;	99US-0154779P.	PI	WPI; 2002-369010/31.	XX
PR	22-SEP-1999;	99US-0155486P.	XX	Identifying plant target proteins for herbicidally active compounds,	XX
PR	24-SEP-1999;	99US-0155659P.	XX	comprising aligning and comparing nucleic acid or amino acid sequences	XX
PR	28-SEP-1999;	99US-0156458P.	XX	from plant with nucleic acid or amino acid sequences from non-plant	XX
PR	29-SEP-1999;	99US-0156596P.	PT	organisms.	XX
PR	04-OCT-1999;	99US-0157117P.	PT	Claim 5; SEQ ID NO 3206; 261pp + Sequence Listing; English.	XX
PR	08-OCT-1999;	99US-0157753P.	XX	The invention relates to identifying target proteins (ABB90790-ABB94016)	XX
PR	06-OCT-1999;	99US-0157865P.	XX	for herbicidally active compounds, comprising aligning and comparing	XX
PR	07-OCT-1999;	99US-0158029P.	XX	nucleic acid or amino acid sequences from plant with nucleic acid or	XX
PR	08-OCT-1999;	99US-0158232P.	XX	amino acid sequences from non-plant organisms using suitable search	XX
PR	12-OCT-1999;	99US-0158369P.	CC	parameters, where plant sequences having an E-value greater by a factor	XX
PR	13-OCT-1999;	99US-0159293P.	CC	of 3 than the E-value of most similar non-plant sequences are selected.	XX
PR	13-OCT-1999;	99US-0159294P.	CC	The polypeptides or nucleic acids encoding them are useful for	XX
PR	14-OCT-1999;	99US-0159332P.	CC	identifying modulators. The identified modulators are useful as	XX
PR	14-OCT-1999;	99US-0159330P.	CC	herbicides	XX
PR	14-OCT-1999;	99US-0159331P.	CC	Sequence 355 AA;	XX
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 Matches 14; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

[illegible]

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 21:58:31 ; Search time 40.2 Seconds
(without alignments)
74.038 Million cell updates/sec

Title: US-10-751-235-11

Perfect score: 177

Sequence: 1 MESSLSPSSSSSYSLFTAKPRLSPKPFPSIR 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75.5	42.7	386	2	US-09-338-420-2
2	59.5	33.6	319	2	US-10-159-901-57
3	54.5	30.8	159	2	US-09-248-796A-21631
4	54	30.5	117	2	US-09-248-796A-23978
5	53.5	30.2	169	2	US-09-248-796A-21929
6	53.5	30.2	1564	2	US-09-487-558B-244
7	53	29.9	829	1	US-08-346-455B-34
8	53	29.9	829	2	US-08-977-221-34
9	53	29.9	829	2	US-09-483-831B-34
10	53	29.9	829	4	PCT-US95-06613-34
11	53	29.9	915	1	US-08-346-455B-69
12	53	29.9	915	2	US-08-977-221-69
13	53	29.9	915	2	US-09-483-831B-69
14	53	29.9	915	4	PCT-US95-06613-69
15	53	29.9	1971	1	US-09-914-272A-1
16	53	29.9	1971	2	US-10-638-333-1
17	53	29.9	1971	2	US-10-747-133A-1
18	52.5	29.7	288	2	US-09-270-767-42632
19	51	28.8	72	2	US-09-107-433-2902
20	51	28.8	119	2	US-09-270-767-35788
21	51	28.8	119	2	US-09-270-767-51005
22	50	28.2	688	2	US-09-489-039A-9153
23	49.5	28.0	680	1	US-08-542-363-4
24	49.5	28.0	680	2	US-09-100-089-4
25	49.5	28.0	680	2	US-09-670-827-4
26	49.5	28.0	680	2	US-09-827-949-4
27	49.5	28.0	1620	1	US-08-542-363-2

Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 381, App
Sequence 299, App
Sequence 18792, A
Sequence 22818, A
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 2, Appli
Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-338-420-2
; Sequence 2, Application US/09338420
; Patent No. 6271445
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Guyer, David
; APPLICANT: Potter, Sharon
; APPLICANT: Subramanian, Mani
; APPLICANT: Walters, Eric
; TITLE OF INVENTION: Methods to screen herbicidal compounds
; TITLE OF INVENTION: and uses thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6271445artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6271445th Carolina
; COUNTRY: USA
; ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,420
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,895
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stulte, Larry W
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: CGC1999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-338-420-2

Query Match 42.7%; Score 75.5; DB 2; Length 386;
Best Local Similarity 48.6%; Pred. No. 0.017;
Matches 17; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

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Qy 1 MESSLFPSSSSSYSLFTAKPTRLSPKPKFTFSI 35
Db 1 MEARIQSSSSSYSLTYVNRSFSPKP-----FSV 32

RESULT 2
US-10-159-901-57
; Sequence 57, Application US/10159901
; Patent No. 6887688
; GENERAL INFORMATION:
; APPLICANT: LAGARIAS, JOHN
; APPLICANT: KOICHI, TAKAYUKI
; APPLICANT: FRANKENBERG, NICOLE
; APPLICANT: GAMBETTA, GREGORY
; APPLICANT: MONTGOMERY, BERONDA
; TITLE OF INVENTION: LIGHT CONTROLLED GENE EXPRESSION UTILIZING HETEROLOGOUS PHYTOCHROME
; CURRENT APPLICATION NUMBER: US/10/159,901
; PRIOR FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-159-901-57

Query Match 33.6%; Score 59.5; DB 2; Length 319;
Best Local Similarity 43.8%; Pred. No. 2.3;
Matches 14; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

Qy 3 SSLFSPSSSSSYSLFTAKPTRL---LSPKPKF 31
Db 7 NTLSSSSPSYSLPTLSKPSKSNLRPAQF 38

RESULT 3
US-09-248-796A-21631
; Sequence 21631, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21631
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21631

Query Match 30.8%; Score 54.5; DB 2; Length 159;
Best Local Similarity 37.8%; Pred. No. 5.1;
Matches 14; Conservative 6; Mismatches 10; Indels 7; Gaps 1;

Qy 3 SSLFSPSSSSSYSLFTAK-----PTRLSPKPKFT 32
Db 17 SKISPSLSSITTTTAEDSINDLPTNVIPTPKTT 53

RESULT 4
US-09-248-796A-23978
; Sequence 23978, Application US/09248796A

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; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23978
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23978

Query Match 30.5%; Score 54; DB 2; Length 117;
Best Local Similarity 41.0%; Pred. No. 4.1;
Matches 16; Conservative 5; Mismatches 12; Indels 6; Gaps 2;

Qy 3 SSLFSPSSSSSYSL-FTAKPTRL-----SPKPKFTFSI 35
Db 25 SFLSQHSSKSYIHFTMIPTIRLLNGAKNVKPLTVPV 63

RESULT 5
US-09-248-796A-21929
; Sequence 21929, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21929
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21929

Query Match 30.2%; Score 53.5; DB 2; Length 169;
Best Local Similarity 34.1%; Pred. No. 7.6;
Matches 15; Conservative 9; Mismatches 7; Indels 13; Gaps 2;

Qy 2 ESSLF-----SPSSSSSYSLFTAK-----PTRLSPKPKFT 32
Db 25 KSIYLTKRLSPSLSSITTTTAEDSINDLPTNVIPTPKTT 68

RESULT 6
US-09-487-558B-244
; Sequence 244, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John

```

APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558B
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0
SEQ ID NO 244
LENGTH: 1564
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-244

Query Match 30.28; Score 53.5; DB 2; Length 1564;
Best Local Similarity 37.57; Pred. No. 1.1e+02;
Matches 12; Conservative 9; Mismatches 8; Indels 3; Gaps 1;

QY 4 SLFSPSSSSSYSLFTAKPTRLSPKPKFTFSI 35
DB 612 SLYRPSADASTFSDVPTKLT---AVTFNI 640

RESULT 7
US-08-346-455B-34
Sequence 34, Application US/08346455B
Patent No. 5731167
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-346-455B-34

Query Match 29.9%; Score 53; DB 1; Length 829;
Best Local Similarity 48.0%; Pred. No. 59;
Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 6 FSPSSSSSYSLFT--AKPTRLSPK 28
DB 235 FGPESSYSGSPFPKPKPKVAPK 259

RESULT 8
US-08-977-221-34
Sequence 34, Application US/08977221
Patent No. 6084069
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 829
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Melanoma
 CELL LINE: A2058
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: Putative protein
 OTHER INFORMATION: sequence of A2058 Autotoxin
 US-08-977-221-34

Query Match 29.9%; Score 53; DB 2; Length 829;
 Best Local Similarity 48.0%; Pred. No. 59;
 Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

Qy 6 FSPSSSYSLFT--AKPTLLSPK 28
 Db 235 FGPESSYSGPFTPAKPKRKVAPK 259

RESULT 9
 US-09-483-831B-34
 Sequence 34, Application US/09483831B
 Patent No. 6417338
 GENERAL INFORMATION:
 APPLICANT: STRACKE, MARY
 APPLICANT: LIOTTA, LANCE
 APPLICANT: SCHIFFMANN, ELLIOTT
 APPLICANT: KRUTZCH, HENRY
 APPLICANT: MURATA, JUN
 TITLE OF INVENTION: AUTOTOXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
 TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
 FILE REFERENCE: 2026-4149US4
 CURRENT APPLICATION NUMBER: US/09/483.831B
 CURRENT FILING DATE: 2000-01-17
 PRIOR APPLICATION NUMBER: 07/822,043
 PRIOR FILING DATE: 1992-01-17
 PRIOR APPLICATION NUMBER: 08/249,182
 PRIOR FILING DATE: 1994-05-25
 PRIOR APPLICATION NUMBER: 08/346,455
 PRIOR FILING DATE: 1994-11-28
 PRIOR APPLICATION NUMBER: 08/977,221
 PRIOR FILING DATE: 1997-11-24
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 34
 LENGTH: 829
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Putative protein sequence of A2058 Autotoxin
 US-09-483-831B-34

Query Match 29.9%; Score 53; DB 2; Length 829;
 Best Local Similarity 48.0%; Pred. No. 59;
 Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

Qy 6 FSPSSSYSLFT--AKPTLLSPK 28
 Db 235 FGPESSYSGPFTPAKPKRKVAPK 259

RESULT 10
 PCT-US95-06613-34
 Sequence 34, Application PC/TUS9506613
 GENERAL INFORMATION:
 APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
 APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
 APPLICANT: HENRY; MURATA, JUN
 TITLE OF INVENTION: MOTILITY STIMULATING
 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 TITLE OF INVENTION: THERAPY
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 829
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Melanoma
 CELL LINE: A2058
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: Putative protein
 OTHER INFORMATION: sequence of A2058 Autotoxin

PCT-US95-06613-34

Query Match 29.9%; Score 53; DB 4; Length 829;
Best Local Similarity 48.0%; Pred. No. 59;
Matches 12; Conservative 3; Mismatches 8; Indels 8; Gaps 1;

QY 6 FSPSSSYSLFT--AKPTLLSPK 28
Db 235 FGPESSYSGPFTPAKPKRKVAPK 259

RESULT 11

US-08-346-455B-69
; Sequence 69, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346.455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: No
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:

US-08-346-455B-69

Query Match 29.9%; Score 53; DB 1; Length 915;
Best Local Similarity 48.0%; Pred. No. 67;
Matches 12; Conservative 3; Mismatches 8; Indels 8; Gaps 1;

QY 6 FSPSSSYSLFT--AKPTLLSPK 28
Db 235 FGPESSYSGPFTPAKPKRKVAPK 259

RESULT 12

US-08-977-221-69
; Sequence 69, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: No
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:

US-08-977-221-69

Query Match 29.9%; Score 53; DB 2; Length 915;
Best Local Similarity 48.0%; Pred. No. 67;
Matches 12; Conservative 3; Mismatches 8; Indels 8; Gaps 1;

QY 6 FSPSSSYSLFT--AKPTLLSPK 28
Db 321 FGPESSYSGPFTPAKPKRKVAPK 345

RESULT 13

US-08-977-221-69
; Sequence 69, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: No
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:

US-08-977-221-69

Query Match 29.9%; Score 53; DB 2; Length 915;
Best Local Similarity 48.0%; Pred. No. 67;
Matches 12; Conservative 3; Mismatches 8; Indels 8; Gaps 1;

QY 6 FSPSSSYSLFT--AKPTLLSPK 28
Db 321 FGPESSYSGPFTPAKPKRKVAPK 345

```

US-09-483-831B-69
; Sequence 69, Application US/09483831B
; Patent No. 6417338
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY
; APPLICANT: LIOTTA, LANCE
; APPLICANT: SCHIFFMANN, ELLIOTT
; APPLICANT: KRUTZSCH, HENRY
; APPLICANT: MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING PROTEIN USEFUL IN
; TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2026-4149US4
; CURRENT APPLICATION NUMBER: US/09/483,831B
; CURRENT FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: 07/822,043
; PRIOR FILING DATE: 1992-01-17
; PRIOR APPLICATION NUMBER: 08/249,182
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/346,455
; PRIOR FILING DATE: 1994-11-28
; PRIOR APPLICATION NUMBER: 08/977,221
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 69
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Polypeptide
US-09-483-831B-69

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```

Query Match 29.9%; Score 53; DB 2; Length 915;
Best Local Similarity 48.0%; Pred. No. 67;
Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

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Qy 6 FSPSSSYSLFT--AKPTLLSPK 28
Db 321 FGPESSYSGPFTPAKPKKVKAPK 345

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RESULT 14
PCT-US95-06613-69
; Sequence 69, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
PCT-US95-06613-69

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```

Query Match 29.9%; Score 53; DB 4; Length 915;
Best Local Similarity 48.0%; Pred. No. 67;
Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

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Qy 6 FSPSSSYSLFT--AKPTLLSPK 28
Db 321 FGPESSYSGPFTPAKPKKVKAPK 345

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RESULT 15
US-09-914-272A-1
; Sequence 1, Application US/09914272A
; Patent No. 6673913
; GENERAL INFORMATION:
; APPLICANT: Sakaguchi, No. 6673913uo
; APPLICANT: Kuwahara, Kazuhiko
; TITLE OF INVENTION: GANP Protein
; FILE REFERENCE: 050208-0014
; CURRENT APPLICATION NUMBER: US/09/914,272A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/JP99/04634
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 47035/1999
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1971
; TYPE: PRT
; ORGANISM: Mouse
US-09-914-272A-1

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Query Match 29.9%; Score 53; DB 2; Length 1971;
Best Local Similarity 38.9%; Pred. No. 1.7e+02;
Matches 14; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

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Qy 1 MESSLPSSSSSYSLFTAKPTLLSPKPKFTSIR 36
Db 231 VSTAFGSSNSSEFTPTASFGSLGEPFANKPSLR 266

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Search completed: March 7, 2006, 22:00:14
Job time : 40.2 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2006, 22:00:32 ; Search time 15.6 Seconds
(without alignments)
46.155 Million cell updates/sec

Title: US-10-751-235-11

Perfect score: 177
Sequence: 1 MESSLPSPSSSYSLFTAKPTLLSPKPTFSIR 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	29.9	352	6	US-10-838-616-4
2	53	29.9	639	7	US-11-094-586-2
3	53	29.9	1971	7	US-11-179-624-1
4	48.5	27.4	505	7	US-11-087-099-6346
5	48.5	27.4	1905	6	US-10-877-346-44
6	48	27.1	527	7	US-11-240-341-44
7	48	27.1	1053	6	US-10-517-939-52
8	48	27.1	1142	7	US-11-044-051-73
9	47.5	26.8	312	7	US-11-072-512-3588
10	47.5	26.8	797	6	US-10-514-531-5
11	47.5	26.8	798	6	US-10-514-531-2
12	47	26.6	130	6	US-10-793-626-164
13	47	26.6	161	7	US-11-087-099-2465
14	47	26.6	688	7	US-11-165-226-124
15	47	26.6	908	7	US-11-087-099-11997
16	47	26.6	1199	6	US-10-821-234-1126
17	47	26.6	1972	7	US-11-124-367A-446
18	46.5	26.3	199	6	US-10-714-887-238
19	46.5	26.3	285	7	US-11-072-512-3028
20	46.5	26.3	680	6	US-10-467-962B-101
21	46	26.0	1890	7	US-11-033-039-314
22	45	25.4	120	6	US-10-915-161-20
23	45	25.4	366	6	US-10-524-647-126
24	45	25.4	366	6	US-10-524-972-114
25	45	25.4	565	6	US-10-915-161-2

26	45	25.4	723	7	US-11-072-512-2246	Sequence 2246, Ap
27	45	25.4	2725	7	US-11-113-424-52	Sequence 52, Appl
28	45	25.4	2725	7	US-11-100-640-10	Sequence 10, Appl
29	45	25.4	2725	7	US-11-100-640-16	Sequence 16, Appl
30	44.5	25.1	175	6	US-10-821-234-1543	Sequence 1543, Ap
31	44.5	25.1	179	7	US-11-197-133A-62	Sequence 62, Appl
32	44.5	25.1	838	7	US-11-114-906-40	Sequence 40, Appl
33	44.5	25.1	851	7	US-11-114-906-38	Sequence 38, Appl
34	44.5	25.1	863	7	US-11-114-906-32	Sequence 32, Appl
35	44.5	25.1	876	7	US-11-114-906-30	Sequence 30, Appl
36	44.5	25.1	951	7	US-11-114-906-36	Sequence 36, Appl
37	44.5	25.1	957	7	US-11-114-906-34	Sequence 34, Appl
38	44.5	25.1	976	7	US-11-114-906-28	Sequence 28, Appl
39	44.5	25.1	982	7	US-11-114-906-26	Sequence 26, Appl
40	44.5	25.1	1027	7	US-11-024-959-324	Sequence 324, App
41	44.5	25.1	1730	7	US-11-182-016-19	Sequence 19, Appl
42	44	24.9	384	7	US-11-134-563-2	Sequence 2, Appl
43	44	24.9	2344	6	US-10-330-773-627	Sequence 627, App
44	43.5	24.6	71	7	US-11-207-078-331	Sequence 331, App
45	43.5	24.6	108	6	US-10-793-626-2898	Sequence 2898, Ap

ALIGNMENTS

RESULT 1

US-10-838-616-4
; Sequence 4, Application US/10838616
; Publication No. US2006008874A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: CREELMAN, Robert A
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal I
; APPLICANT: REUBER, T. Lynne
; TITLE OF INVENTION: Plant Transcriptional Regulators of Abiotic Stress
; FILE REFERENCE: MBI-0069CIP
; CURRENT APPLICATION NUMBER: US/10/838,616
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: Stress-Related Polypeptides in Plants
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/685,922
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 09/810,836
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G9 polypeptide Paralogous to G867, G993, G1930
US-10-838-616-4

Query Match 29.9% Score 53; DB 6; Length 352;


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; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 1905
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-10-877-346-44

Query Match      27.1%; Score 48.5; DB 6; Length 1905;
Best Local Similarity 38.7%; Pred. No. 1.4e+02;
Matches 12; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

Qy      1 MESSLPSSSSVSLTAKPTRLSPKPKF 31
Db      254 LDTQLTSPDSTG-EQFFTSKIVRLCVDDPKF 283

RESULT 6
US-11-240-341-44
; Sequence 44, Application US/11240341
; Publication No. US20060024742A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Valerie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Fallex, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461.700470US01
; CURRENT APPLICATION NUMBER: US/11/240,341
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/183,789
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 09/060,706
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-240-341-44

Query Match      27.1%; Score 48; DB 7; Length 527;
Best Local Similarity 42.9%; Pred. No. 39;
Matches 12; Conservative 5; Mismatches 7; Indels 4; Gaps 1;

Qy      8 PSSSSVSLTAKPT----RLSPKPKF 31
Db      496 PTTESRALFGDKPTIKQPMILRLKPKF 523

RESULT 7
US-10-517-939-52
; Sequence 52, Application US/10517939
; Publication No. US2006003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 56446200701
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
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; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1053
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(30)
; US-10-517-939-52

Query Match      27.1%; Score 48; DB 6; Length 1053;
Best Local Similarity 42.9%; Pred. No. 84;
Matches 15; Conservative 4; Mismatches 4; Indels 12; Gaps 3;

Qy      6 FSPSSSSVSLTAKPT----LLSPK-PKFTFSI 35
Db      159 FSPS-----FESTTKCSLIVVSPKNSFTFYI 186

RESULT 8
US-11-044-051-73
; Sequence 73, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisla
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-044-051-73

Query Match      27.1%; Score 48; DB 7; Length 1142;
Best Local Similarity 33.3%; Pred. No. 92;
Matches 13; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

Qy      1 MESSLPSSSSVSSYS----SLTAKPTRLSPKPKFTFSI 35
Db      124 VQSPLOQNPASSFFSALLSIFQSSPSIQSPFEGPQSV 162

RESULT 9
US-11-072-512-3588
; Sequence 3588, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
```

```
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHUKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTUYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3588
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-514-531-2

Query Match      26.8%; Score 47.5; DB 7; Length 312;
Best Local Similarity 40.7%; Pred. No. 25;
Matches 11; Conservative 4; Mismatches 9; Indels 3; Gaps 1;

QY      7 SPSSSSYSSSLF---KPTRLSPKPK 30
Db      238 SPDSEGLSSVSSSLPFTNSSSPSR 264

RESULT 10
US-10-514-531-5
; Sequence 5, Application US/10514531
; Publication No. US20060035849A1
; GENERAL INFORMATION:
; APPLICANT: Spiegelman, Bruce M., et al.
; TITLE OF INVENTION: Methods and Compositions For Modulating Type I Muscle
; FILE REFERENCE: DFN-041US
; CURRENT APPLICATION NUMBER: US/10/514,531
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: PCT/US03/04792
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 60/357069
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-514-531-5

Query Match      26.8%; Score 47.5; DB 6; Length 797;
Best Local Similarity 35.7%; Pred. No. 72;
Matches 15; Conservative 6; Mismatches 8; Indels 13; Gaps 2;

QY      4 SLF--SPSSSSYS-----SLFTAKPTRLSPKPKFT 32
Db      531 SLFDVSPSCSFSNCPDRSVSPKSLFQRPQMRSRSRFS 572

RESULT 11
US-10-514-531-2
; Sequence 2, Application US/10514531
; Publication No. US20060035849A1
; GENERAL INFORMATION:
; APPLICANT: Spiegelman, Bruce M., et al.
; TITLE OF INVENTION: Methods and Compositions For Modulating Type I Muscle
; FILE REFERENCE: DFN-041US
; CURRENT APPLICATION NUMBER: US/10/514,531
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: PCT/US03/04792
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 60/357069
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-514-531-2

Query Match      26.8%; Score 47.5; DB 6; Length 798;
Best Local Similarity 35.7%; Pred. No. 72;
Matches 15; Conservative 6; Mismatches 8; Indels 13; Gaps 2;

QY      4 SLF--SPSSSSYS-----SLFTAKPTRLSPKPKFT 32
Db      532 SLFNVSPSCSFSNCPDRSVSPKSLFQRPQMRSRSRFS 573

RESULT 12
US-10-793-626-164
; Sequence 164, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-164

Query Match      26.6%; Score 47; DB 6; Length 130;
Best Local Similarity 42.4%; Pred. No. 11;
Matches 14; Conservative 5; Mismatches 4; Indels 10; Gaps 2;

QY      3 SSLSFSPSSSSYSLSLFTAKPTRLSPKPKFTFSI 35
Db      66 STVHKFSSST-STLYT-----KPKLTISI 88

RESULT 13
US-11-087-099-2465
; Sequence 2465, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2465
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-11-087-099-2465
```

Search completed: March 7, 2006, 22:06:39
Job time : 16.6 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 21:53:39 ; Search time 28.8 Seconds
(without alignments)
120.271 Million cell updates/sec

Title: US-10-751-235-11
Perfect score: 177
Sequence: 1 MESSLSPSSSSSYSLFTAKPTLLSPKPKFTFSIR 36
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	177	100.0	566	2 T46159	cytochrome P450-11
2	65.5	37.0	430	2 T50296	conserved hypotet
3	60	33.9	355	1 J02256	phosphoribosylform
4	60	33.9	389	2 T47440	phosphoribosylform
5	59.5	33.6	319	2 A85437	hypothetical prote
6	58.5	33.1	351	2 T19059	hypothetical prote
7	56	31.6	474	2 T45818	hypothetical prote
8	56	31.6	883	2 S04722	puff 74E protein
9	55	31.1	406	2 T48103	mRNA binding prote
10	54.5	30.8	612	2 T38714	hypothetical prote
11	54.5	30.8	1621	2 T30200	protein-tyrosine k
12	54	30.5	132	2 A75491	hypothetical prote
13	54	30.5	205	2 T47591	aintegumenta-like
14	54	30.5	403	2 T45712	NAD-dependent mala
15	54	30.5	403	2 T51862	malate dehydrogena
16	53.5	30.2	1564	2 S55317	probable transport
17	53	29.9	352	2 T51330	DNA binding protei
18	53	29.9	915	1 A55344	autotaxin precurs
19	52.5	29.7	402	2 A84766	hypothetical prote
20	52.5	29.7	411	2 T51818	ATP phosphoribosyl
21	52	29.4	159	2 D71033	hypothetical prote
22	52	29.4	246	2 T30490	hypothetical prote
23	52	29.4	320	2 T31547	hypothetical prote
24	52	29.4	2606	2 T03159	large tegument pro
25	51.5	29.1	272	2 H71124	hypothetical prote
26	51	28.8	211	2 C84751	hypothetical prote
27	51	28.8	299	2 T52452	ATP-dependent Clp
28	51	28.8	354	2 T49806	hypothetical prote
29	51	28.8	446	2 T45525	WSC4 homolog limpo

30 51 28.8 499 2 AH3323 UDP-N-acetylmuramo
31 51 28.8 620 2 S52494 protein kinase hom
32 51 28.8 2305 2 B89608 protein C23P12.1 l
33 51 28.8 2305 2 T15571 hypothetical prote
34 50.5 28.5 361 2 T01998 hypothetical prote
35 50.5 28.5 632 2 T00679 hypothetical prote
36 50.5 28.5 960 2 S54461 hypothetical prote
37 50.5 28.5 1390 2 T18883 hypothetical prote
38 50 28.2 291 2 E84849 hypothetical prote
39 50 28.2 562 2 T05758 hypothetical prote
40 50 28.2 687 2 AE0345 polyphosphate kina
41 50 28.2 688 2 AC0819 polyporphosphate kina
42 50 28.2 707 2 T14195 extensin homolog T
43 50 28.2 848 2 E86443 probable G-protein
44 50 28.2 1695 2 T19823 hypothetical prote
45 49.5 28.0 113 2 F72746 hypothetical prote

ALIGNMENTS

RESULT 1
T46159
Cytochrome P450-like protein - Arabidopsis thaliana
N;Alternate names: protein T4D2.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46159
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23025
A;Accession: T46159
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-566 <N>A>
A;Cross-references: UNIPROT:Q9SCP8; UNIPARC:UPI000009D7F9; EMBL:AL132958
A;Experimental source: cultivar Columbia; BAC clone T4D2
C;Genetics:
A;Map position: 3
A;Introns: 183/2; 292/3; 358/3; 392/3; 439/3; 475/3; 503/2; 557/3
A;Note: T4D2.60
C;Superfamily: pea cytochrome P450 CYP97; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;371-536/Domain: cytochrome P450 homology <P45>
F;514/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 177; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 1e-15; 0; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0;

QY 1 MESSLSPSSSSSYSLFTAKPTLLSPKPKFTFSIR 36
|||||
DB 1 MESSLSPSSSSSYSLFTAKPTLLSPKPKFTFSIR 36
|||||

RESULT 2

T50296
conserved hypothetical SH3 domain protein [imported] - fission yeast (Schizosaccharomyces
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50296
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, December 1999
A;Reference number: Z25040
A;Accession: T50296
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-430 <NCD>
A;Cross-references: UNIPROT:Q9URW6; UNIPARC:UPI000006AE4A; EMBL:AL133359; PIDN:CAB62422.1
A;Experimental source: strain 972h(-)
C;Genetics:
A;Gene: SPDB:SPAPJ696.02.
A;Map position: 1

QY 3 SSLSFSPSSSS-----YSSLFTAK-----PTRLSPKPKFTFS 34
Db 73 SSMFAASSPSAAATYSTVTAAALVVPFTLQSPKREFVCS 111

RESULT 7

T45818
hypothetical protein F2809.250 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45818
R;Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23014
A;Accession: T45818
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <BN>
A;Cross-references: UNIPROT:Q9M2K7; UNIPARC:UPI00000A7FBF; EMBL:AL137080
A;Experimental source: cultivar Columbia; BAC clone F2809
C;Genetics:
A;Map position: 3
A;Note: F2809.250
C;Superfamily: Arabidopsis thaliana hypothetical protein F2809.250

Query Match 31.6%; Score 56; DB 2; Length 474;
Best Local Similarity 48.5%; Pred. No. 10;
Matches 16; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 7 SPSSSSYS-----SLFTAKPTRLSPKPKFTFSI 35
Db 33 SPSSSSSPATTLFRSRRLLSKAQSTISI 65

RESULT 8

S04722
puff 74E protein - fruit fly (Drosophila melanogaster)
N;Alternate names: ecdysone-induced protein E74B; ets-related protein E74B
C;Species: Drosophila melanogaster
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04722; B34692
R;Janknecht, R.; Taube, W.; Lueddecke, H.J.; Pongs, O.
Nucleic Acids Res. 17, 4455-4464, 1989
A;Title: Characterization of a putative transcription factor gene expressed in the 20-OH
A;Reference number: S04722; MUID:89315191; PMID:2501755
A;Accession: S04722
A;Molecule type: DNA
A;Residues: 1-883 <JAN>
A;Cross-references: UNIPROT:P11536; UNIPARC:UPI0000129AFF; EMBL:X15087; NID:g7513; PIDN:
R;Burtis, K.C.; Thummel, C.S.; Jones, C.W.; Katim, F.D.; Hogness, D.S.
Cell 61, 85-99, 1990
A;Title: The Drosophila 74EF early puff contains E74, a complex ecdysone-inducible gene
A;Reference number: A90912; MUID:90199900; PMID:2107982
A;Accession: B34692
A;Molecule type: DNA
A;Residues: 1-866, 'Q', 868-883 <BUR>
A;Cross-references: UNIPARC:UPI00001247C8; GB:M37083; NID:g157309; PID:g157310
C;Genetics:
A;Gene: FlyBase:Bip74EF
A;Cross-references: FlyBase:FBgn0000567
A;Map position: 3 74EF
C;Keywords: alternative splicing; DNA binding; transcription regulation
F;789-869/Domain: ets DNA-binding domain homology <ETS>

Query Match 31.6%; Score 56; DB 2; Length 883;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 SSLSFSPSSSSYSLSFTAKPTRLSP 27
Db 39 SSLSLSSSSSSSSLSATPTPVASP 63

RESULT 9

T48103
mRNA binding protein CSP41 homolog T20010.240 [similarity] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48103
R;Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeidler, K.; Mewes, H.W.; Rudd, S.; Lem
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24484
A;Accession: T48103
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-406 <OBE>
A;Cross-references: UNIPROT:Q9LYA9; UNIPARC:UPI000009DBE02; EMBL:AL163816
A;Experimental source: cultivar Columbia; BAC clone T20010

C;Genetics:
A;Map position: 3
A;Introns: 132/3; 173/2; 207/3; 254/1; 346/3
A;Note: T20010.240

Query Match 31.1%; Score 55; DB 2; Length 406;
Best Local Similarity 58.1%; Pred. No. 12;
Matches 18; Conservative 4; Mismatches 7; Indels 2; Gaps 2;

QY 3 SSLSFSPSSSSYSLSL-FTAKPTRLSPKPKFT 32
Db 41 SSLSSSSSSSSSLSLTSRLTSRLSPQ-KFT 70

RESULT 10

T38714
hypothetical protein SPAC3F10.13 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38714
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z21807
A;Accession: T38714
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-612 <MUR>
A;Cross-references: UNIPROT:Q10187; UNIPARC:UPI000013A1B8; EMBL:Z69369; PIDN:CAA93311.1;
A;Experimental source: strain 972h; cosmid c3F10

C;Genetics:
A;Gene: SPDB:SPAC3F10.13
A;Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC3F10.13

Query Match 30.8%; Score 54.5; DB 2; Length 612;
Best Local Similarity 32.6%; Pred. No. 22;
Matches 14; Conservative 7; Mismatches 13; Indels 9; Gaps 1;

QY 3 SSLSFSPSSSSYSLSL-FTAKPTRLSPKPKFTFSIR 36
Db 234 SSYFSPNAEFDFSTGLSSLTNSKPTVIFNFKPNSTPDLR 276

RESULT 11

T30200
protein-tyrosine kinase (EC 2.7.1.112) alk - mouse
N;Alternate names: anaplastic lymphoma kinase
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30200
R;Iwahara, T.; Fujimoto, J.; Wen, D.; Cupples, R.; Bucay, N.; Arakawa, T.; Mori, S.; Rat
Oncogene 14, 439-449, 1997
A;Title: Molecular characterization of ALK, a receptor tyrosine kinase expressed specif
A;Reference number: Z20774; MUID:97178863; PMID:9053841

A;Accession: T30200
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

Job time : 30.8 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 21:43:16 ; Search time 178.2 Seconds
(without alignments)
142.531 Million cell updates/sec

Title: US-10-751-235-11

Perfect score: 177

Sequence: 1 MESSLSPSSSSSYSLFTAKPTRLSPKPKFTFSIR 36

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	177	100.0	539	2	Q6TDX7 ARATH
2	177	100.0	552	2	Q8RWV4 ARATH
3	177	100.0	566	2	Q9SCP8 ARATH
4	65.5	37.0	430	2	Q9URW6 SCHPO
5	62.5	35.3	1332	2	Q8MQQ8 DROME
6	62.5	35.3	2016	2	Q9VLS7 DROME
7	61.5	34.7	1383	2	Q5BIU5 EMENI
8	60	33.9	389	1	PUR5 ARATH
9	59.5	33.6	319	1	RCCR ARATH
10	59	33.3	624	2	Q7S9T0 NEUCR
11	59	33.3	1545	2	Q9VYN1 DROME
12	59	33.3	1733	2	Q4HAD7 MOUSE
13	58.5	33.1	355	2	Q17793 CAEEL
14	58	32.8	605	2	Q75WN1 CHAOB
15	58	32.8	771	2	Q86H13 DICDI
16	58	32.8	2408	2	Q57UP3 9TRYP
17	57.5	32.5	512	2	Q55P26 CRYNE
18	57.5	32.5	513	2	Q5KSD0 CRYNE
19	57	32.2	126	2	Q69316 CRYHO
20	57	32.2	144	2	Q4XCA2 PLACH
21	57	32.2	302	2	Q9CS59 ARATH
22	57	32.2	1449	2	Q86A82 DICDI
23	57	32.2	1464	2	Q55X33 DICDI
24	56.5	31.9	497	2	Q6MAZ9 PARUM
25	56.5	31.9	577	2	Q62000 CAEBR
26	56	31.6	353	2	Q8XON1 NEUCR
27	56	31.6	357	2	Q9D347 MOUSE
28	56	31.6	434	2	Q8LED3 ARATH
29	56	31.6	459	2	Q5P245 MOUSE
30	56	31.6	474	2	Q9M2K7 ARATH
31	56	31.6	476	2	Q8W418 ARATH

32	56	31.6	497	2	Q6PDE7 MOUSE
33	56	31.6	883	1	E74EB DROME
34	56	31.6	1061	2	Q55SD2 DICDI
35	56	31.6	1806	2	Q869R4 DICDI
36	55	31.1	143	2	Q8LA28 ARATH
37	55	31.1	406	2	Q9LYA9 ARATH
38	55	31.1	818	2	Q6J735 SORBI
39	55	31.1	836	2	Q4RM98 TETNG
40	54.5	30.8	138	2	Q62F09 ORYSA
41	54.5	30.8	416	2	Q6Z8R9 ORYSA
42	54.5	30.8	612	1	UCP6 SCHPO
43	54.5	30.8	696	2	Q86ZL2 PODAN
44	54.5	30.8	1621	1	ALK_MOUSE
45	54.5	30.8	2027	1	DOCK3_MOUSE

ALIGNMENTS

RESULT 1
Q6TDX7 ARATH
ID Q6TDX7 ARATH PRELIMINARY; PRT; 539 AA.
AC Q6TDX7;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Chloroplast carotenoid epsilon-ring hydroxylase.
GN Names=LUT1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14709673; DOI=10.1073/pnas.2237237100;
RA Tian L., Musetti V., Kim J., Magallanes-Lundback M., DellaPenna D.;
RT "The Arabidopsis LUT1 locus encodes a member of the cytochrome P450
family that is required for carotenoid epsilon-ring hydroxylation
activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:402-407(2004).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AY424805; AAR83120.1; -; mRNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00463; EP4501.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
KW Transmembrane.
SQ SEQUENCE 539 AA; 60555 MW; 4C25C728B676ABEB CRC64;

Query Match 100.0%; Score 177; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 9.8e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSLSPSSSSSYSLFTAKPTRLSPKPKFTFSIR 36
|||||
Db 1 MESSLSPSSSSSYSLFTAKPTRLSPKPKFTFSIR 36

RESULT 2
Q8RWV4 ARATH
ID Q8RWV4 ARATH PRELIMINARY; PRT; 552 AA.
AC Q8RWV4;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Putative cytochrome P450 (Fragment).

GN Name=At3G53130;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eudicots II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; AY091083; AML13903.1; -; mRNA.
 DR HSSP; P14779; 1UPZ.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR PRINTS; PR00463; P4501.
 DR Pfam; PF00067; P450.1.
 DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
 DR Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
 KW Transmembrane. 1
 FT NON_TER 1
 SQ SEQUENCE 552 AA; 62073 MW; C23CF8498B5B8440 CRC64;

 Query Match 100.0%; Score 177; DB 2; Length 552;
 Best Local Similarity 100.0%; Pred. No. 1e-14;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MESSLFPSSSSSYSLFTAKPTLLSPKPKFTFSIR 36
 Db 14 MESSLFPSSSSSYSLFTAKPTLLSPKPKFTFSIR 49

 RESULT 3
 Q9SCP8 ARATH PRELIMINARY; PRT; 566 AA.
 AC Q9SCP8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cytochrom P450-like protein.
 GN Name=T4D2.60;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eudicots II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
 RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
 RA Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; ALI32958; CAB64216.1; -; Genomic_DNA.
 DR HSSP; P14779; 1UPZ.
 DR GO; GO:0004497; F:metal ion binding; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR PRINTS; PR00463; P450.1.
 DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
 KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
 KW Transmembrane. 566 AA; 63596 MW; B884E8996B1A4C7D CRC64;
 SQ SEQUENCE 566 AA; 63596 MW; B884E8996B1A4C7D CRC64;

 Query Match 100.0%; Score 177; DB 2; Length 566;
 Best Local Similarity 100.0%; Pred. No. 1e-14;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MESSLFPSSSSSYSLFTAKPTLLSPKPKFTFSIR 36
 Db 1 MESSLFPSSSSSYSLFTAKPTLLSPKPKFTFSIR 36

 RESULT 4
 Q9URW6 SCHPO PRELIMINARY; PRT; 430 AA.
 ID Q9URW6 SCHPO PRELIMINARY;
 AC Q9URW6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE SPAPJ696.02 protein.
 GN ORFNames=SPAPJ696.02;
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
 RA Wood V., Williams R., Rajadream M.A., Lyne M.H., Lyne R., Stewart A.,
 RA Sgouras J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K.L., Murphy D., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer C., Holzer D.,
 RA Hilbert H., Borzym K., Langer I., Beck A., Leirach H., Reinhardt R.,
 RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Spakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "the genome sequence of Schizosaccharomycetes pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 DR EMBL; ALI33359; CAB62422.1; -; Genomic_DNA.
 DR PIR; T50296; T50296.
 DR HSSP; P08631; 1RU1.
 DR GeneDB_Spombe; SPAPJ696.02; -.
 DR InterPro; IPR007462; DUF500.
 DR Pfam; PF04366; DUF500; 1.
 DR Pfam; PF00018; SH3_1; 1.


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DR PRINTS: PR00452; SH3DOMAIN.
DR PRODOM: ED000066; SH3; 1.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PSS0002; SH3; 1.
DR KW Complete proteome; SH3 domain.
DR SQ SEQUENCE 430 AA; 46373 MW; AC300C08C29D946F CRC64;

Query Match 37.08; Score 65.5; DB 2; Length 430;
Best Local Similarity 55.28; Pred. No. 4.4;
Matches 16; Conservative 2; Mismatches 6; Indels 5; Gaps 1;

QY 3 SSLSFSPSSSSYSLFTAKPRLLSPKPF 31
Db 343 SSQFSRSSYS-----KPSRTPAKPKF 366

RESULT 5
Q8MQ08 DROME PRELIMINARY; PRT; 1332 AA.
AC Q8MQ08;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE L21041p (Fragment).
GN ORFNames=CG8552;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RA Chapeton M., Brokstein J., Hong L., Agbayani A., Carlson J.,
RA George R., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL EMBL: AY128444; AA75037.1; -; mRNA.
DR Ensembl; CG8552; Drosophila melanogaster.
DR Flybase; FBgn0031990; CG8552.
DR GO; GO:0046872; F-metal ion binding; IEA.
DR InterPro; IPR004177; DDHD.
DR Pfam; PF02862; DDHD; 1.
DR Pfam; PF02825; WWE; 1.
DR PROSITE; PSS0918; WWE; 1.
FT NON TER 1
SQ SEQUENCE 1332 AA; 144944 MW; B3P3F5931D907008 CRC64;

Query Match 35.38; Score 62.5; DB 2; Length 1332;
Best Local Similarity 47.48; Pred. No. 41;
Matches 18; Conservative 4; Mismatches 11; Indels 5; Gaps 2;

QY 3 SSLSFSPSSSSYSLFTAKP-----TRLLSPKPKFTFSI 35
Db 302 SSLSFSPQVDSLSLFPPTTSANTTILTPADTTSTL 339

RESULT 6
Q9VLS7 DROME PRELIMINARY; PRT; 2016 AA.
AC Q9VLS7;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Names=CG8552; ORFNames=CG8552;
GN Drosophila melanogaster (Fruit fly).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein J., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cavenot E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Waberman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.E., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

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RESULT 9	RCR_ARATH	STANDARD;	PRT;	319 AA.
ID	RCR_ARATH	STANDARD;	PRT;	319 AA.
AC	Q8LDU4; O23185;			
AT	10-OCT-2003 (Rel. 42, Created)			
CT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Red chlorophyll catabolite reductase, chloroplast precursor			
DE	(BC 1.-.-.-) (RCR reductase) (ATRCR) (Accelerated cell death protein			
DE	2).			
GN	Name=RCR; Synonyms=ACD2; OrderedLocusNames=At4g37000;			
GN	ORFNames=C7A10.360;			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
OC	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
OC	NCBI_TaxID=3702;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.			
RC	STRAIN=cv. Columbia;			
RC	MEDLINE=20208062; PubMed=10743659;			
RC	Wuehrich K.L., Bovet L., Hunziker P.E., Donnison I.S.,			
RC	Hoertensteiner S.;			
RT	"Molecular cloning, functional expression and characterization of RCR			
RT	reductase, involved in chlorophyll catabolism.";			
RT	Plant J. 21:189-198 (2000).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE, SUBCELLULAR LOCATION, AND MUTANTS ACD2-7;			
RP	ACD2-12E13 AND ACD2-6/ACD2-8.			
RC	STRAIN=cv. Columbia;			
RC	MEDLINE=21143384; PubMed=1149948; DOI=10.1073/pnas.021452998;			
RC	Mach J.M., Castillo A.R., Hoogerstraten R., Greenberg J.T.;			
RT	"The Arabidopsis accelerated cell death gene ACD2 encodes red			
RT	chlorophyll catabolite reductase and suppresses the spread of disease			
RT	symptoms.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 98:771-776 (2001).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=cv. Columbia;			
RC	MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;			
RC	Mayer K.F.X., Schueller C., Wambutt R., Entian K.-D., Terryn N.,			
RA	Fohl T., Duescherhoef A., Stiekema W., Entian K.-D., Terryn N.,			
RA	Harris B., Anorge W., de Simone V., Obermaier L.A., Rieger M.,			
RA	Weichselgartner M., de Brandt P., Grivell L.A., Rieger M.,			
RA	Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidheini T.,			
RA	Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,			
RA	Vos P., Hohseil J., Zimmermann W., Wedler H., Ridley P.,			
RA	Langham S.-A., McCullagh B., Bilham L., Robben J.,			
RA	Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,			
RA	Braeken M., Weltjens I., Voet M., Bastiaens U., Hilbert H., Braun M.,			
RA	Weitzneger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,			
RA	Holzer E., Brandt A., Peters S., van Staveren M., Dirks W.,			
RA	Moolenaar P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,			
RA	Bernisei S., Hempel S., Feldpausch M., Lamberth S., van den Daele H.			
RA	De Keyser A., Buysschaert C., Gielen J., Villarroel R., De Clercq R.,			
RA	Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,			
RA	Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlay K., Mayes R.			
RA	Petrett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,			
RA	Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,			
RA	Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,			
RA	Gabel C., Fuchs M., Farmann B., Granderath K., Dauner D., Herzl A.,			
RA	Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,			
RA	Massenet O., Quigley F., Cibaoud G., Muendlein A., Felber R.,			
RA	Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,			
RA	Chetoui F., Cooke R., Berger C., Monfort A., Casacuberta E.,			
RA	Gibbons T., Weber N., Vandenbol M., Barges M., Torol J., Torres A.,			
RA	Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,			
RA	Heinen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke K.,			
RA	Friedman D., Haase D., Lemcke K., Meves H.-W., Stocker S.,			
RA	Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,			
RA	Farnell L., Dedha N., Gnoj L., Schutz K., Huang E., Spiegel L.,			
RA	Sekton M., Murray J., Sheet P., Cordes M., Abu-Theid J.,			
RA	Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,			

RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., L.W.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana";
RL Nature 402:769-777 (1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome.";
RL Science 302:842-846 (2003).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.A.;
RT "Full-length cDNA from Arabidopsis thaliana";
CC Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the key reaction of chlorophyll catabolism,
CC porphyrin macrocycle cleavage of pheophorbide a (pheide a) to a
CC primary fluorescent catabolite (pFCC). Works in a two-step
CC reaction with pheophorbide a oxygenase (PaO) by reducing the
CC C20/C1 double bond of the intermediate, RCC.
CC -!- COFACTOR: reduced ferredoxin.
CC -!- PATHWAY: Chlorophyll degradation; fourth step.
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma, and a low amount in
CC mitochondria of 7-day-old seedlings.
CC -!- TISSUE SPECIFICITY: Expressed in all tissues tested, including
CC roots.
CC -!- DEVELOPMENTAL STAGE: Present at all times of development. No
CC change of levels during senescence or pathogen attack.
CC -!- MISCELLANEOUS: The absence of light completely suppresses cell
CC death in acd2 mutants.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF326347; AAC53980.1; -; mRNA.
CC EMBL; Z99707; CAB16763.1; -; Genomic DNA.
CC EMBL; AY045578; CAB80366.1; -; Genomic DNA.
CC EMBL; AY045578; AAK73936.1; -; mRNA.
CC EMBL; AY093785; AAM10401.1; -; mRNA.
CC EMBL; AY085797; AAM63013.1; -; mRNA.
CC InterPro; IPR009439; RCC_reductase.
CC Pfam; PF06405; RCC_reductase; 1.
CC Chlorophyll catabolism; Chloroplast; Coiled coil; Oxidoreductase;
KW Transit peptide.
FT TRANSIT 1 39 Chloroplast (Potential).
FT CHAIN 40 319 Red chlorophyll catabolite reductase.
FT COILED 255 286 Potential.

PT MUTAGEN 140 140 G->V: In acd2-12E13; spontaneous
PT spreading cell death lesions.
PT Missing: In acd2-7; spontaneous spreading
PT cell death lesions.
PT R->K: In acd2-6; spontaneous spreading
PT cell death lesions.
PT D -> E (in Ref. 5).
SQ SEQUENCE 319 AA; 36449 MW; A46DC65FB7452517 CRC64;
Query Match 33.6%; Score 59.5; DB 1; Length 319;
Best Local Similarity 43.8%; Pred. No. 19;
Matches 14; Conservative 7; Mismatches 8; Indels 3; Gaps 1;
Qy 3 SSLFSPSSSSSYSLFTAKPTL---LSPKPKF 31
Db 7 NTLYSSSSSYLSPLTSKPSKFNLPRAQF 38
RESULT 10
Q7S910_NEUCR PRELIMINARY; PRT; 624 AA.
AC Q7S910;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU06547.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels W., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Tanakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kanvyssellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Siller S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000213; EAA33018.1; -; Genomic DNA.
SQ SEQUENCE 624 AA; 65243 MW; 54F90D3DC73605C CRC64;
Query Match 33.3%; Score 59; DB 2; Length 624;
Best Local Similarity 51.9%; Pred. No. 49;
Matches 14; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
Qy 3 SSLFSPSSSSSYSLFTAKPTLRLSPKP 29
Db 287 SSSSSSSSSSSSAFSSLSLTFSP 313
RESULT 11
Q9VYN1_DROME PRELIMINARY; PRT; 1545 AA.
ID Q9VYN1_DROME PRELIMINARY;
AC Q9VYN1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CG11245-PA.

GN Name=CG11245; ORFNames=CG11245;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liao X., Leiby Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleab J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
melanogaster euchromatic genome sequence.";
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleab J., Park S., Swirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003489; AAF48161.1; -; Genomic DNA.
DR Ensembl; CG11245; *Drosophila melanogaster*.
DR FlyBase; FBgn0030388; CG11245.
SQ SEQUENCE 1545 AA, 166082 MW, 2ABCEABED136C888 CRC64;
Query Match 33.3%; Score 59; DB 2; Length 1545;
Best Local Similarity 44.1%; Pred. No. 1.4e+02;
Matches 15; Conservative 3; Mismatches 12; Indels 4; Gaps 1;
QY 2 ESSLFSPSSSSVSSSLFTAKPTRLSPKPTFSI 35
DB 475 ESLLIQFLTSGSGSSSTPTP-----SPKPKFTVNV 504
RESULT 12
Q4HAD7_MOUSE PRELIMINARY; PRT; 1733 AA.
AC Q4HAD7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE ATP-binding cassette (ABC) transporter ABCA14.
GN Name=ABCA14;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6N; TISSUE=Testis;
RA Ban N., Sasaki M., Sakai H., Ueda K., Inagaki N.;
RT "Cloning of ABCA17, a novel rodent sperm-specific ABC (ATP-binding
cassette) transporter that regulates intracellular lipid metabolism.";
RL Biochem. J. 389:577-585 (2005).
DR EMBL; AB112584; BAD97416.1; -; mRNA.
KW ATP-binding.
SQ SEQUENCE 1733 AA, 195943 MW, 2D4DB5B8D19F6D6E CRC64;
Query Match 33.3%; Score 59; DB 2; Length 1733;
Best Local Similarity 44.8%; Pred. No. 1.6e+02;
Matches 13; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
QY 2 ESSLFSPSSSSVSSSLFTAKPTRLSPKPK 30
DB 1692 QALASFPSPNSRPISSPPLSLSPK 1720
RESULT 13
Q17793_CAEEL PRELIMINARY; PRT; 355 AA.
ID Q17793_CAEEL PRELIMINARY;
AC Q17793; Q22365;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

Best Local Similarity 51.9%; Pred. No. 85;
Matches 14; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 8 PSSSSYSSLFTAKPTRLSPKPKFTFS 34
||||| ||| |::| |
Db 479 PSSSSSSSSSTTPTSTTTPNSTTS 505

Search completed: March 7, 2006, 21:58:12
Job time : 181.2 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	177	100.0	36	5	US-10-751-235-11	Sequence 11, Appl
2	177	100.0	539	5	US-10-751-235-4	Sequence 4, Appli
3	177	100.0	560	5	US-10-739-930-6317	Sequence 6317, Ap
4	63	35.6	260	4	US-10-310-154-688	Sequence 688, App
5	63	35.6	260	5	US-10-733-923-601	Sequence 601, App
6	63	35.6	262	5	US-10-733-923-21136	Sequence 21136, A
7	62.5	35.3	2016	6	US-11-097-143-18525	Sequence 18525, A
8	61.5	34.7	309	5	US-10-732-923-5867	Sequence 5867, Ap
9	61.5	34.7	424	5	US-10-732-923-5866	Sequence 5866, Ap
10	61	34.5	82	4	US-10-425-115-348345	Sequence 348345, A
11	61	34.5	389	4	US-10-424-599-230527	Sequence 230527,
12	59.5	33.6	319	3	US-09-870-406A-57	Sequence 57, Appl
13	59.5	33.6	319	4	US-10-159-901-57	Sequence 57, Appl
14	59.5	33.6	319	5	US-10-733-930-5731	Sequence 5731, Ap
15	59.5	33.6	525	4	US-10-424-599-260318	Sequence 260318,
16	59	33.3	1545	6	US-11-097-143-23523	Sequence 23523, A
17	58.5	33.1	78	4	US-10-424-599-278783	Sequence 278783,
18	58	32.8	109	4	US-10-425-115-257160	Sequence 257160,
19	58	32.8	131	4	US-10-425-115-257159	Sequence 257159,
20	58	32.8	160	4	US-10-425-115-257153	Sequence 257153,
21	57.5	32.5	215	4	US-10-424-599-201457	Sequence 201457,
22	57.5	32.5	283	4	US-10-424-599-261750	Sequence 261750,
23	56.5	31.9	131	4	US-10-424-599-236698	Sequence 236698,
24	56	31.6	48	5	US-10-450-763-33222	Sequence 35222, A
25	56	31.6	204	4	US-10-424-599-196060	Sequence 196060,
26	56	31.6	883	6	US-11-097-143-13482	Sequence 13482, A
27	55.5	31.4	370	4	US-10-424-599-245828	Sequence 245828,

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; ORGANISM: Arabidopsis thaliana
US-10-751-235-4

Query Match      100.0%; Score 177; DB 5; Length 539;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSLFSPSSSSYSYLFTAKPTRLSPKPKFTFSIR 36
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Db 1 MESSLFSPSSSSYSYLFTAKPTRLSPKPKFTFSIR 36
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RESULT 3
US-10-739-930-6317
; Sequence 6317, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6317
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: ARATH-23APR03-C3001_1.p
US-10-739-930-6317

Query Match      100.0%; Score 177; DB 5; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSLFSPSSSSYSYLFTAKPTRLSPKPKFTFSIR 36
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Db 22 MESSLFSPSSSSYSYLFTAKPTRLSPKPKFTFSIR 57
   |||||

RESULT 4
US-10-310-154-688
; Sequence 688, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.

```

APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21136
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(262)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-21136

Query Match 35.6%; Score 63; DB 5; Length 262;
Best Local Similarity 46.2%; Pred. No. 5.8;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 10 SSSVSLFTAKPTLLSPKPKFTFSI 35
Db 4 SATSASLFSANPTPLFSKPSLSLHL 29

RESULT 7
US-11-097-143-18525
; Sequence 18525, Application US/11097143
; Publication No. US20050208559A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18525
; LENGTH: 2016
; TYPE: PRT
; ORGANISM: DROSOPHILA

Query Match 35.3%; Score 62.5; DB 6; Length 2016;
Best Local Similarity 47.4%; Pred. No. 65;
Matches 18; Conservative 4; Mismatches 11; Indels 5; Gaps 2;

QY 3 SSLFSPSS-SSYSLSFTAKE-TRLLSPKPKFTFSI 35
Db 986 SSLFSPSQVDSLSLFPAPPTSANTILTPADTTSTL 1023

RESULT 8
US-10-732-923-5867
; Sequence 5867, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 5867
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(309)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-5867

Query Match 34.7%; Score 61.5; DB 5; Length 309;
Best Local Similarity 43.8%; Pred. No. 11;
Matches 14; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 2 ESSLFSPSSSSYSLFTAKPTLLSP-KPKFT 32
Db 31 DSYMATPSSSYASSFAASPLPTTAPASPSFS 62

RESULT 9
US-10-732-923-5866
; Sequence 5866, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 5866
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(424)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-5866

Query Match 34.7%; Score 61.5; DB 5; Length 424;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 14; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 2 ESSLFSPSSSSYSLFTAKPTLLSP-KPKFT 32
Db 150 DSYMATPSSSYASSFAASPLPTTAPASPSFS 181

RESULT 10
US-10-425-115-348345
; Sequence 348345, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ;; TITLE OF INVENTION: Plants
 ;; FILE REFERENCE: 38-21(53222)B
 ;; CURRENT APPLICATION NUMBER: US/10/425,115
 ;; CURRENT FILING DATE: 2003-04-28
 ;; NUMBER OF SEQ ID NOS: 369326
 ;; SEQ ID NO 348345
 ;; LENGTH: 82
 ;; TYPE: PRT
 ;; ORGANISM: Zea mays
 ;; FEATURE:
 ;; OTHER INFORMATION: Clone ID: MRT4577_80854C.1.pcp
 US-10-425-115-348345

Query Match 34.5%; Score 61; DB 4; Length 82;
 Best Local Similarity 43.5%; Pred. No. 2.9;
 Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 13 YSSLFTAKPTLLSPKPKFTFSI 35
 Db 59 HKKIFSLNPTKILIPTRVTFSI 81

RESULT 11
 US-10-424-599-230527
 ; Sequence 230527, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 230527
 ; LENGTH: 389
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_50188C.1.pcp
 US-10-424-599-230527

Query Match 34.5%; Score 61; DB 4; Length 389;
 Best Local Similarity 46.9%; Pred. No. 16;
 Matches 15; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 3 SSSLFSPSSSYSSLFTAKPTLLSPKPKFTFS 34
 Db 50 SSCSPSAAGSSSPSPFRLRLPKPTAFS 81

RESULT 12
 US-09-870-406A-57
 ; Sequence 57, Application US/09870406A
 ; Publication No. US20030104379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAGARIAS, JOHN
 ; APPLICANT: KOICHI, TAKAYUKI
 ; APPLICANT: FRANKENBERG, NICOLE
 ; APPLICANT: GAMBETTA, GREGORY
 ; APPLICANT: MONTGOMERY, BERONDA
 ; TITLE OF INVENTION: HY2 FAMILY OF BILIN REDUCTASES
 ; FILE REFERENCE: 407T-907720US
 ; CURRENT APPLICATION NUMBER: US/09/870,406A
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 60/271,758
 ; PRIOR FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 60/210,286
 ; PRIOR FILING DATE: 2000-06-08

;; NUMBER OF SEQ ID NOS: 57
 ;; SOFTWARE: PatentIn version 3.0
 ;; SEQ ID NO 57
 ;; LENGTH: 319
 ;; TYPE: PRT
 ;; ORGANISM: Arabidopsis thaliana
 US-09-870-406A-57

Query Match 33.6%; Score 59.5; DB 3; Length 319;
 Best Local Similarity 43.8%; Pred. No. 20;
 Matches 14; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

Qy 3 SSSLFSPSSSYSSLFTAKPTLLSPKPKF 31
 Db 7 NTLYSSSPSYLSPLTSKPSRFSKNLRPRAQF 38

RESULT 13
 US-10-159-901-57
 ; Sequence 57, Application US/10159901
 ; Publication No. US2003007235A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAGARIAS, JOHN
 ; APPLICANT: KOICHI, TAKAYUKI
 ; APPLICANT: FRANKENBERG, NICOLE
 ; APPLICANT: GAMBETTA, GREGORY
 ; APPLICANT: MONTGOMERY, BERONDA
 ; TITLE OF INVENTION: LIGHT CONTROLLED GENE EXPRESSION UTILIZING HETEROLOGOUS PHYTOCHRON
 ; FILE REFERENCE: 407T-907731US
 ; CURRENT APPLICATION NUMBER: US/10/159,901
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: 60/294,463
 ; PRIOR FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 57
 ; LENGTH: 319
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-159-901-57

Query Match 33.6%; Score 59.5; DB 4; Length 319;
 Best Local Similarity 43.8%; Pred. No. 20;
 Matches 14; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

Qy 3 SSSLFSPSSSYSSLFTAKPTLLSPKPKF 31
 Db 7 NTLYSSSPSYLSPLTSKPSRFSKNLRPRAQF 38

RESULT 14
 US-10-739-930-5731
 ; Sequence 5731, Application US/10739930
 ; Publication No. US20040216190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
 ; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53377)B
 ; CURRENT APPLICATION NUMBER: US/10/739,930
 ; CURRENT FILING DATE: 2003-12-18
 ; NUMBER OF SEQ ID NOS: 11088
 ; SEQ ID NO 5731
 ; LENGTH: 319
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: ARATH-23APR03-C1272_1.p
 US-10-739-930-5731

Query Match 33.6%; Score 59.5; DB 5; Length 319;
 Best Local Similarity 43.8%; Pred. No. 20;
 Matches 14; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

Qy		3 SSI FSPSSSSSYSSLFAKPTRL---LSPKPF 31 : :
Dd		7 NTL YSSSSPSYLSPLTSKPFRFSKNLFPRAOF 38 : :

RESULT 15

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US-10-424-599-260318
; Sequence 260318, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 260318
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(525)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_77090C.1.pep
US-10-424-599-260318

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Query Match 33.6%; Score 59.5; DB 4; Length 525;
Best Local Similarity 40.0%; Pred. NO. 36;
Matches 14; Conservative 9; Mismatches 7; Indels 5; Gaps 2;

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QY      5 LFPSSSSSYSLF--TAKPTRLL---SPKPKFTFS 34
          :::| |::: : | | | : | | | | :
Dd     49 IYTPKSPSFTSVLDSSGKNORLLVPSTPKPKFIET 83
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Search completed: March 7, 2006, 22:04:14
Job time : 140.4 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 8, 2006, 11:24:53 ; Search time 165 Seconds
(without alignments)
25.323 Million cell updates/sec

Title: US-10-751-235-14
Perfect score: 33
Sequence: 1 FXGXGXXCXG 10

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap:
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap:
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4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap:
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6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	10	3	US-09-739-254-129
2	33	100.0	10	3	US-09-904-615-129
3	33	100.0	10	4	US-10-067-534-15
4	33	100.0	10	4	US-10-210-965-5
5	33	100.0	10	4	US-10-054-988-129
6	33	100.0	10	4	US-10-236-433-11
7	33	100.0	10	5	US-10-477-526-7
8	33	100.0	10	5	US-10-477-526-8
9	33	100.0	10	5	US-10-751-235-14
10	33	100.0	10	5	US-10-751-235-15
11	33	100.0	11	4	US-10-097-559-28
12	33	100.0	11	5	US-10-804-772-26
13	33	100.0	11	5	US-10-804-772-29
14	33	100.0	14	4	US-10-373-877-10
15	33	100.0	14	4	US-10-373-877-19
16	33	100.0	14	4	US-10-373-877-20
17	33	100.0	14	4	US-10-373-877-21
18	33	100.0	14	4	US-10-373-877-22
19	33	100.0	14	4	US-10-373-877-23
20	33	100.0	14	4	US-10-373-877-24
21	33	100.0	14	4	US-10-373-877-25
22	33	100.0	14	5	US-10-865-478-774
23	33	100.0	15	3	US-09-957-674-13
24	33	100.0	15	4	US-10-257-378-1
25	33	100.0	15	5	US-10-882-241-17
26	33	100.0	16	4	US-10-163-198-90
27	33	100.0	16	5	US-10-926-683-1257

28	33	100.0	18	2	US-08-647-444-12	Sequence 12, Appl
29	33	100.0	20	5	US-10-855-595-6	Sequence 6, Appl
30	33	100.0	20	5	US-10-855-595-7	Sequence 7, Appl
31	33	100.0	20	5	US-10-855-595-8	Sequence 8, Appl
32	33	100.0	20	5	US-10-855-595-9	Sequence 9, Appl
33	33	100.0	20	5	US-10-855-595-10	Sequence 10, Appl
34	33	100.0	20	5	US-10-855-532-6	Sequence 6, Appl
35	33	100.0	20	5	US-10-855-532-7	Sequence 7, Appl
36	33	100.0	20	5	US-10-855-532-8	Sequence 8, Appl
37	33	100.0	20	5	US-10-855-532-9	Sequence 9, Appl
38	33	100.0	20	5	US-10-855-532-10	Sequence 10, Appl
39	33	100.0	21	4	US-10-021-425-25	Sequence 25, Appl
40	33	100.0	21	5	US-10-900-856-28	Sequence 28, Appl
41	33	100.0	23	4	US-10-103-196-31	Sequence 31, Appl
42	33	100.0	30	3	US-09-749-637A-126	Sequence 126, App
43	33	100.0	30	3	US-09-749-637A-129	Sequence 129, App
44	33	100.0	30	3	US-09-749-637A-283	Sequence 283, App
45	33	100.0	30	4	US-10-433-485A-1	Sequence 1, Appl
46	33	100.0	30	5	US-10-839-227-126	Sequence 126, App
47	33	100.0	30	5	US-10-839-227-129	Sequence 129, App
48	33	100.0	30	5	US-10-839-227-283	Sequence 283, App
49	33	100.0	32	4	US-10-437-963-159510	Sequence 159510,
50	33	100.0	35	4	US-10-351-641-487	Sequence 487, App
51	33	100.0	35	4	US-10-351-641-488	Sequence 488, App
52	33	100.0	35	4	US-10-351-641-489	Sequence 489, App
53	33	100.0	35	4	US-10-351-641-490	Sequence 490, App
54	33	100.0	35	4	US-10-351-641-491	Sequence 491, App
55	33	100.0	35	4	US-10-351-641-492	Sequence 492, App
56	33	100.0	35	4	US-10-351-641-493	Sequence 493, App
57	33	100.0	35	4	US-10-351-641-523	Sequence 523, App
58	33	100.0	35	4	US-10-351-641-524	Sequence 524, App
59	33	100.0	35	4	US-10-351-641-525	Sequence 525, App
60	33	100.0	35	4	US-10-351-641-526	Sequence 526, App
61	33	100.0	35	4	US-10-351-641-527	Sequence 527, App
62	33	100.0	35	4	US-10-351-641-528	Sequence 528, App
63	33	100.0	35	4	US-10-351-641-529	Sequence 529, App
64	33	100.0	39	4	US-10-147-140-54	Sequence 54, Appl
65	33	100.0	40	3	US-09-894-882-348	Sequence 348, App
66	33	100.0	40	3	US-09-894-882-482	Sequence 482, App
67	33	100.0	40	5	US-10-894-314A-347	Sequence 347, App
68	33	100.0	41	4	US-10-894-314A-482	Sequence 482, App
69	33	100.0	41	4	US-10-425-115-244467	Sequence 244467,
70	33	100.0	42	4	US-10-424-599-143366	Sequence 143366,
71	33	100.0	42	4	US-10-424-599-256014	Sequence 256014,
72	33	100.0	42	4	US-10-425-115-238482	Sequence 238482,
73	33	100.0	43	4	US-10-424-599-187772	Sequence 187772,
74	33	100.0	44	4	US-10-424-599-271553	Sequence 271553,
75	33	100.0	44	4	US-10-425-115-239272	Sequence 239272,
76	33	100.0	46	4	US-10-267-682-208	Sequence 208, App
77	33	100.0	46	4	US-10-267-748-208	Sequence 208, App
78	33	100.0	49	4	US-10-424-599-157117	Sequence 157117,
79	33	100.0	49	4	US-10-425-115-238518	Sequence 238518,
80	33	100.0	49	4	US-10-425-115-240869	Sequence 240869,
81	33	100.0	49	4	US-10-425-115-324478	Sequence 324478,
82	33	100.0	50	4	US-10-425-115-351931	Sequence 351931,
83	33	100.0	50	4	US-10-425-115-260285	Sequence 260285,
84	33	100.0	51	4	US-10-424-599-167757	Sequence 167757,
85	33	100.0	51	4	US-10-424-599-177489	Sequence 177489,
86	33	100.0	51	4	US-10-424-599-214094	Sequence 214094,
87	33	100.0	52	3	US-09-864-761-45740	Sequence 45740, A
88	33	100.0	52	4	US-10-424-599-254214	Sequence 254214,
89	33	100.0	52	5	US-10-926-683-1061	Sequence 1061, Ap
90	33	100.0	54	4	US-10-424-599-273991	Sequence 273991,
91	33	100.0	54	4	US-10-437-963-185080	Sequence 185080,
92	33	100.0	55	3	US-09-864-761-34668	Sequence 34668, A
93	33	100.0	55	4	US-10-106-698-6891	Sequence 6891, Ap
94	33	100.0	55	4	US-10-425-115-250988	Sequence 250988,
95	33	100.0	56	4	US-10-425-115-361393	Sequence 361393,
96	33	100.0	57	4	US-10-424-599-199843	Sequence 199843,
97	33	100.0	57	4	US-10-425-115-261158	Sequence 261158,
98	33	100.0	59	4	US-10-424-599-176580	Sequence 176580,
99	33	100.0	59	4	US-10-425-115-280265	Sequence 280265,
100	33	100.0	59	4	US-10-425-115-314843	Sequence 314843,

Kavali

ALIGNMENTS

RESULT 1
US-09-739-254-129
; Sequence 129, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/739,254
; CURRENT FILING DATE: 2000-12-19
; EARLIER APPLICATION NUMBER: 09/511,554
; EARLIER FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: PCT/US99/19330
; EARLIER FILING DATE: 1998-08-24
; EARLIER APPLICATION NUMBER: 60/097,917
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/098,634
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-739-254-129

Query Match 100.0%; Score 33; DB 3; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 1 FSLGRRHCLG 10

RESULT 2
US-09-904-615-129
; Sequence 129, Application US/09904615
; Patent No. US20020026040A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-615-129

Query Match 100.0%; Score 33; DB 3; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 1 FSLGRRHCLG 10

RESULT 3

US-10-067-534-15
; Sequence 15, Application US/10067534
; Publication No. US20020187538A1
; GENERAL INFORMATION:
; APPLICANT: Esenberg, Margaret K.
; APPLICANT: Chen, Xiao-Ya
; APPLICANT: Luo, Ping
; APPLICANT: Wang, Yan-Hong
; TITLE OF INVENTION: cDNA Clone of (+)-Delta-Cadinene-8-Hydroxylase Gene from Cotton
; FILE REFERENCE: 006602-113
; CURRENT APPLICATION NUMBER: US/10/067,534
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/267,160
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Gossypium arboreum
US-10-067-534-15

Query Match 100.0%; Score 33; DB 4; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 1 FGSGRRMCAG 10

RESULT 4

US-10-210-965-5
; Sequence 5, Application US/10210965
; Publication No. US20030078404A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 33297, A Human Cytochrome P450 Family
; FILE REFERENCE: MP101-091P1RM
; CURRENT APPLICATION NUMBER: US/10/210,965
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/312428
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus pattern, Prosite Accession No. US20030078404A1 PS000086
; FEATURE:
; OTHER INFORMATION: Phe can be Trp.
; LOCATION: 1
; NAME/KEY: VARIANT
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 2
; OTHER INFORMATION: Ser can be Gly, Asn, or His.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa can be any amino acid.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Gly can be Asp.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 5
; OTHER INFORMATION: Xaa can be any amino acid.

FEATURE:
NAME/KEY: VARIANT
LOCATION: (6)...(6)
OTHER INFORMATION: Arg can be Lys, His, Pro, or Thr.
FEATURE:
NAME/KEY: VARIANT
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa can be any amino acid.
FEATURE:
NAME/KEY: VARIANT
LOCATION: (8)...(8)
OTHER INFORMATION: Cys is involved in binding heme iron
FEATURE:
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Leu can be Ile, Val, Met, Phe, Ala, or Pro.
FEATURE:
NAME/KEY: VARIANT
LOCATION: (10)...(10)
OTHER INFORMATION: Gly can be Ala or Asp.
US-10-210-965-5

Query Match 100.0%; Score 33; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 1 FSXGXXXCXG 10

RESULT 5

US-10-054-988-129
Sequence 129, Application US/10054988
Publication No. US20030087341A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: P2032P1
CURRENT APPLICATION NUMBER: US/10/054,988
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 09/904,615
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 129
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-054-988-129

Query Match 100.0%; Score 33; DB 4; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 1 FSLGRRXCXG 10

RESULT 6

US-10-236-433-11
Sequence 11, Application US/10236433
Publication No. US2003010025A1
GENERAL INFORMATION:
APPLICANT: O'Connor, Michael B.
APPLICANT: Gilbert, Lawrence I.

APPLICANT: Warren, James T.
TITLE OF INVENTION: Insecticide Targets
FILE REFERENCE: 09531-07001
CURRENT APPLICATION NUMBER: US/10/236,433
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/318,006
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/317,890
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: P450 motif
FEATURE:
NAME/KEY: VARIANT
LOCATION: 2,3,5,6,7,9
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-236-433-11

Query Match 100.0%; Score 33; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 1 FXXGXXXCXG 10

RESULT 7

US-10-477-526-7
Sequence 7, Application US/10477526
Publication No. US2005009021A1
GENERAL INFORMATION:
APPLICANT: Wisniewski, Jan
APPLICANT: Ramshaw, Heather
APPLICANT: Petkovich, Martin P.
TITLE OF INVENTION: A Retinoic Acid Metabolizing Cytochrome P450
FILE REFERENCE: 11812-91
CURRENT APPLICATION NUMBER: US/10/477,526
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US 60/292,531
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent in version 3.1
SEQ ID NO 7
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (2)...(3)
OTHER INFORMATION: x=any residue
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: x=any residue
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (5)...(7)
OTHER INFORMATION: x=any residue
US-10-477-526-7

Query Match 100.0%; Score 33; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 1 FXXGXXXCXG 10

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RESULT 8
US-10-477-526-8
; Sequence 8, Application US/10477526
; Publication No. US2005009021A1
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; APPLICANT: Ramshaw, Heather
; APPLICANT: Petkovich, Martin P.
; TITLE OF INVENTION: A Retinoic Acid Metabolizing Cytochrome P450
; FILE REFERENCE: 11812-91
; CURRENT APPLICATION NUMBER: US/10/477,526
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/292,531
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-477-526-8

Query Match      100.0%; Score 33; DB 5; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|:|:|:|:|:|
Db 1 FGGGRRSLG 10

RESULT 9
US-10-751-235-14
; Sequence 14, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: Dellapenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(7)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-751-235-14

Query Match      100.0%; Score 33; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
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```
Db 1 FXXGXXXCXG 10
|:|:|:|:|:|

RESULT 10
US-10-751-235-15
; Sequence 15, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: Dellapenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-751-235-15

Query Match      100.0%; Score 33; DB 5; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|:|:|:|:|:|
Db 1 FSGGPRKCVG 10

RESULT 11
US-10-097-559-28
; Sequence 28, Application US/10097559
; Publication No. US20030166255A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: Ralston, Lyle F.
; TITLE OF INVENTION: Cytochrome P450s and Uses Thereof
; FILE REFERENCE: 07678/100003
; CURRENT APPLICATION NUMBER: US/10/097,559
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 60/274,241
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/275,597
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum p450 protein
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4,8
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-097-559-28

Query Match      100.0%; Score 33; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|:|:|:|:|:|
Db 2 FGKGRXCPG 11

RESULT 12
US-10-804-772-26
; Sequence 26, Application US/10804772
```

Publication No. US20040244077A1
 GENERAL INFORMATION:
 APPLICANT: Azpiroz, Ricardo
 APPLICANT: Choe, Sunghwa
 APPLICANT: Feldmann, Kenneth A.
 TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
 FILE REFERENCE: 11696-070001
 CURRENT APPLICATION NUMBER: US/10/804,772
 CURRENT FILING DATE: 2004-03-18
 PRIOR APPLICATION NUMBER: US/09/502,426
 PRIOR FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: US 60/119,657
 PRIOR FILING DATE: 1999-02-11
 PRIOR APPLICATION NUMBER: US 60/119,658
 PRIOR FILING DATE: 1999-02-11
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: Fast-Seq for Windows Version 4.0
 SEQ ID NO 26
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Heme binding domain
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: 4
 OTHER INFORMATION: Xaa = Ala, Ser, or Val
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: 8
 OTHER INFORMATION: Xaa = Any Amino Acid
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: 10
 OTHER INFORMATION: Xaa = Pro, Ala, or Val
 US-10-804-772-26

Query Match 100.0%; Score 33; DB 5; Length 11;
 Best Local Similarity 70.0%; Pred. No. 3.8e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXXXG 10
 Db 2 FGXGRRXXG 11

RESULT 13
 US-10-804-772-29
 Sequence 29, Application US/10804772
 Publication No. US20040244077A1
 GENERAL INFORMATION:
 APPLICANT: Azpiroz, Ricardo
 APPLICANT: Choe, Sunghwa
 APPLICANT: Feldmann, Kenneth A.
 TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
 FILE REFERENCE: 11696-070001
 CURRENT APPLICATION NUMBER: US/10/804,772
 CURRENT FILING DATE: 2004-03-18
 PRIOR APPLICATION NUMBER: US/09/502,426
 PRIOR FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: US 60/119,657
 PRIOR FILING DATE: 1999-02-11
 PRIOR APPLICATION NUMBER: US 60/119,658
 PRIOR FILING DATE: 1999-02-11
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: Fast-Seq for Windows Version 4.0
 SEQ ID NO 29
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Exemplary sequence
 US-10-804-772-29

Query Match 100.0%; Score 33; DB 5; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXXXG 10
 Db 2 FGGGPRLCAG 11

RESULT 14
 US-10-373-877-10
 Sequence 10, Application US/10373877
 Publication No. US20030198986A1
 GENERAL INFORMATION:
 APPLICANT: Lathe, Richard
 APPLICANT: Rose, Kenneth A.
 APPLICANT: Stapleton, Genevieve
 TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
 SEQUENCES CODING THEREFOR AND USED THEREOF
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 No. US20030198986A1 Glebe Rd. 8th floor
 CITY: Arlington
 STATE: VA
 COUNTRY: USA
 ZIP: 22201-4741
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/373,877
 FILING DATE: 27-Feb-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB95/02465
 FILING DATE: 18-OCT-1995
 APPLICATION NUMBER: 09/270,751
 FILING DATE: 17-MAR-1999
 APPLICATION NUMBER: 08/845,161
 FILING DATE: 21-APR-1997
 APPLICATION NUMBER: GB 9421093.7
 FILING DATE: 19-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Mitchard, Leonard C.
 REGISTRATION NUMBER: 29,009
 REFERENCE/DOCKET NUMBER: 604-572
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-816-4000
 TELEFAX: 703-816-4100
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-10-373-877-10

Query Match 100.0%; Score 33; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXXXG 10
 Db 1 FXXGXXXXXG 10

RESULT 15

```
US-10-373-877-19
; Sequence 19, Application US/10373877
; Publication No. US20030198986A1
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
;           Rose, Kenneth A.
;           Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. US20030198986A1th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/373,877
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: 09/270,751
; FILING DATE: 17-MAR-1999
; APPLICATION NUMBER: 08/845,161
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-572
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4100
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
;
; Query Match 100.0%; Score 33; DB 4; Length 14;
; Best Local Similarity 40.0%; Pred. No. 4.7e+02;
; Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 FXXGXXXCXG 10
; Db 1 FGLGTSKCPG 10
;
; RESULT 16
; US-10-373-877-20
; Sequence 20, Application US/10373877
; Publication No. US20030198986A1
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
;           Rose, Kenneth A.
;           Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. US20030198986A1th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/373,877
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: 09/270,751
; FILING DATE: 17-MAR-1999
; APPLICATION NUMBER: 08/845,161
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-572
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4100
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
;
; US-10-373-877-20
;
; Query Match 100.0%; Score 33; DB 4; Length 14;
; Best Local Similarity 40.0%; Pred. No. 4.7e+02;
; Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 FXXGXXXCXG 10
; Db 1 FGSGATCPG 10
;
; RESULT 17
; US-10-373-877-21
; Sequence 21, Application US/10373877
; Publication No. US20030198986A1
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
;           Rose, Kenneth A.
;           Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. US20030198986A1th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/373,877
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: 09/270,751
; FILING DATE: 17-MAR-1999
; APPLICATION NUMBER: 08/845,161
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-572
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
;
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-373-877-21

Query Match 100.0%; Score 33; DB 4; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 1 FGAGPRSCVG 10

RESULT 18
US-10-373-877-22
; Sequence 22, Application US/10373877
; Publication No. US20030198986A1
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard A.
; Rose, Kenneth A.
; Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. US20030198986A1th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/373,877
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: 09/270,751
; FILING DATE: 17-MAR-1999
; APPLICATION NUMBER: 08/845,161
; FILING DATE: 21-APR-1997
```

```
;
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-572
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
;
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-373-877-22

Query Match 100.0%; Score 33; DB 4; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 1 FGFGMRCLG 10

RESULT 19
US-10-373-877-23
; Sequence 23, Application US/10373877
; Publication No. US20030198986A1
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard A.
; Rose, Kenneth A.
; Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. US20030198986A1th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/373,877
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: 09/270,751
; FILING DATE: 17-MAR-1999
; APPLICATION NUMBER: 08/845,161
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-572
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
```

;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-373-877-23

Query Match 100.0%; Score 33; DB 4; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXCXG 10
Db 1 FCGARVCLG 10

RESULT 20

US-10-373-877-24
; Sequence 24, Application US/10373877
; Publication No. US20030198986A1
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard A.
; Rose, Kenneth A.
; Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. US20030198986A1th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/373,877
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: 09/270,751
; FILING DATE: 17-MAR-1999
; APPLICATION NUMBER: 08/845,161
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-572
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Query Match 100.0%; Score 33; DB 4; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXCXG 10
Db 1 FCGARVCLG 10

US-10-373-877-24

Query Match 100.0%; Score 33; DB 4; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXCXG 10
Db 1 FGMGVRQCLG 10

RESULT 21

US-10-373-877-25
; Sequence 25, Application US/10373877
; Publication No. US20030198986A1
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard A.
; Rose, Kenneth A.
; Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. US20030198986A1th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/373,877
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: 09/270,751
; FILING DATE: 17-MAR-1999
; APPLICATION NUMBER: 08/845,161
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-572
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-373-877-25

Query Match 100.0%; Score 33; DB 4; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXCXG 10
Db 1 FGMGVRQCLG 10

RESULT 22

US-10-865-478-774
; Sequence 774, Application US/10865478
; Publication No. US20040235041A1
; GENERAL INFORMATION:

APPLICANT: Shinkets, Richard A.
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: cSingle Nucleotide Polymorphisms for Known Genes
FILE REFERENCE: 15966-534-CIP1
CURRENT APPLICATION NUMBER: US/10/865,478
CURRENT FILING DATE: 2004-06-10
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 09/443,199
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/442,129
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/442,849
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 880
SOFTWARE: CuraGen Patent Formatter Version 0.9
SEQ ID NO 774
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (7)...(0)
OTHER INFORMATION: cSNP translation
US-10-865-478-774

Query Match 100.0%; Score 33; DB 5; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
DB 2 FHYGVLCAG 11

RESULT 23
US-09-957-674-13
Sequence 13, Application US/09957674
Patent No. US20020120948A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Methods for Expressing Gene Products
FILE REFERENCE: 18396/2072
CURRENT APPLICATION NUMBER: US/09/957,674
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: GB990736
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: PCT/GB00/01225
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 15
TYPE: PRT
ORGANISM: Hepatitis B virus
US-09-957-674-13

Query Match 100.0%; Score 33; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
DB 4 FLGGITVCLG 13

RESULT 24
US-10-257-378-1
Sequence 1, Application US/10257378
Publication No. US20030190642A1
GENERAL INFORMATION:
APPLICANT: Jones, Glenville
APPLICANT: Petkovich, P. Martin

APPLICANT: White, Jay
APPLICANT: Ramshaw, Heather A.
APPLICANT: Scangle, Wayne A.
TITLE OF INVENTION: A Thymus Expressed Human Cytochrome P450 (P450TEC)
FILE REFERENCE: 11812-65
CURRENT APPLICATION NUMBER: US/10/257,378
CURRENT FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 60/208,785
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/198,617
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: query sequence
FEATURE:
NAME/KEY: UNSURE
LOCATION: (3)
OTHER INFORMATION: Xaa can be Gly or Ser
FEATURE:
NAME/KEY: UNSURE
LOCATION: (4)
OTHER INFORMATION: Xaa can be any amino acid
FEATURE:
NAME/KEY: UNSURE
LOCATION: (6)
OTHER INFORMATION: Xaa can be any amino acid
FEATURE:
NAME/KEY: UNSURE
LOCATION: (8)
OTHER INFORMATION: Xaa can be any amino acid
FEATURE:
NAME/KEY: UNSURE
LOCATION: (7)
OTHER INFORMATION: Xaa can be Ala, Arg, or His
FEATURE:
NAME/KEY: UNSURE
LOCATION: (10)
OTHER INFORMATION: Xaa can be any amino acid
FEATURE:
NAME/KEY: UNSURE
LOCATION: (12)...(13)
OTHER INFORMATION: Xaa can be amino acid
FEATURE:
NAME/KEY: UNSURE
LOCATION: (14)
OTHER INFORMATION: Xaa can be Phe, Leu, or Ile
US-10-257-378-1

Query Match 100.0%; Score 33; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
DB 2 FXXGXXXCXG 11

RESULT 25
US-10-882-241-17
Sequence 17, Application US/10882241
Publication No. US20050114910A1
GENERAL INFORMATION:
APPLICANT: LONE, YU-CHUN
APPLICANT: PAJOT, ANTHONY
APPLICANT: AURIAULT, CLAUDE
APPLICANT: PANCRE, VERONIQUE
APPLICANT: LEMONNIER, FRANCOIS
TITLE OF INVENTION: TRANSGENIC MICE HAVING A HUMAN MAJOR HISTOCOMPATIBILITY

; TITLE OF INVENTION: COMPLEX (MHC) PHENOTYPE, EXPERIMENTAL USES AND APPLICATIONS
 ; FILE REFERENCE: 03495.0319
 ; CURRENT APPLICATION NUMBER: US/10/882,241
 ; CURRENT FILING DATE: 2004-07-02
 ; PRIOR APPLICATION NUMBER: 60/490,945
 ; PRIOR FILING DATE: 2003-08-05
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 17
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-10-882-241-17

Query Match 100.0%; Score 33; DB 5; Length 15;
 Best Local Similarity 40.0%; Pred. No. 5e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 Db 5 FLGGTTVCLG 14

RESULT 26
 US-10-163-198-90
 ; Sequence 90, Application US/10163198
 ; Publication No. US20030126645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rebecca E. Cahoon
 ; APPLICANT: Elmer P. Heppard
 ; APPLICANT: No. US20030126645A1uhiro Nagasawa
 ; APPLICANT: Hajime Sakai
 ; TITLE OF INVENTION: Alteration Of Embryo/Endosperm Size During Seed Development
 ; FILE REFERENCE: B1487 US NA
 ; CURRENT APPLICATION NUMBER: US/10/163,198
 ; CURRENT FILING DATE: 2002-06-05
 ; PRIOR APPLICATION NUMBER: 60/295,921
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: 60/334,317
 ; PRIOR FILING DATE: 2001-11-28
 ; NUMBER OF SEQ ID NOS: 111
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 90
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: conserved sequence motif
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (9)..(9)
 ; OTHER INFORMATION: Xaa = any amino acid
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (13)..(13)
 ; OTHER INFORMATION: Xaa = any amino acid
 US-10-163-198-90

Query Match 100.0%; Score 33; DB 4; Length 16;
 Best Local Similarity 60.0%; Pred. No. 5.3e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 Db 7 FGXGRXCPCG 16

RESULT 27
 US-10-926-683-1257
 ; Sequence 1257, Application US/10926683
 ; Publication No. US20050106595A1
 ; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert A.
 ; APPLICANT: Giordano J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.025CPI
 ; CURRENT APPLICATION NUMBER: US/10/926,683
 ; CURRENT FILING DATE: 2004-08-25
 ; PRIOR APPLICATION NUMBER: US/09/471,276
 ; PRIOR FILING DATE: 1999-12-21
 ; PRIOR APPLICATION NUMBER: 09/057,719
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 09/069,047
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: PCT/IB99/00712
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 1622
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 1257
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: -14..-1
 US-10-926-683-1257

Query Match 100.0%; Score 33; DB 5; Length 16;
 Best Local Similarity 40.0%; Pred. No. 5.3e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 Db 4 FFGNSPCG 13

RESULT 28
 US-08-647-444-12
 ; Sequence 12, Application US/08647444
 ; Publication No. US20020127548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Seidman, Christine
 ; APPLICANT: Seidman, Jonathan
 ; APPLICANT: Thierfelder, Ludwig
 ; APPLICANT: Watkins, Hugh
 ; APPLICANT: Mcrae, Calum
 ; TITLE OF INVENTION: Methods for Detecting Mutations Associated
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/647,444
 ; FILING DATE: 11-NOV-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elizabeth A. Hanley
 ; REGISTRATION NUMBER: 33,505
 ; REFERENCE/DOCKET NUMBER: IGI-037CP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-647-444-12

Query Match 100.0%; Score 33; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
DB 2 FDGGIYVCG 11

RESULT 29
US-10-855-595-6
Sequence 6, Application US/10855595
Publication No. US20040235057A1
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/855,595
FILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/882,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7
US-10-855-595-7

Query Match 100.0%; Score 33; DB 5; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
DB 2 FSGGAENCIG 11

RESULT 31
US-10-855-595-8
Sequence 8, Application US/10855595
Publication No. US20040235057A1
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West

CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/855,595
FILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/882,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-10-855-595-8
Query Match 100.0%; Score 33; DB 5; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGXGXXCXG 10
Db 2 FSGGRNCIG 11
RESULT 32
US-10-855-595-9
Sequence 9, Application US/10855595
Publication No. US20040235057A1
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/855,595
FILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000

APPLICATION NUMBER: 08/882,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9
US-10-855-595-9
Query Match 100.0%; Score 33; DB 5; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGXGXXCXG 10
Db 2 FGTGPRNCIG 11
RESULT 33
US-10-855-595-10
Sequence 10, Application US/10855595
Publication No. US20040235057A1
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/855,595
FILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/882,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10
US-10-855-595-10

Query Match 100.0%; Score 33; DB 5; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
DB 2 FSGGSRNCIG 11

RESULT 34

US-10-855-532-6

Sequence 6, Application US/10855532
Publication No. US20040259074A1

GENERAL INFORMATION:

APPLICANT: Petkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/855,532
FILING DATE: 28-May-2004

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/882,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653

INFORMATION FOR SEQ ID NO: 6

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-10-855-532-6

Query Match 100.0%; Score 33; DB 5; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
DB 2 FGGGRLCPG 11

RESULT 35

US-10-855-532-7

Sequence 7, Application US/10855532
Publication No. US20040259074A1

GENERAL INFORMATION:

APPLICANT: Petkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/855,532
FILING DATE: 28-May-2004

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/882,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653

INFORMATION FOR SEQ ID NO: 7

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7
US-10-855-532-7

Query Match 100.0%; Score 33; DB 5; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
DB 2 FSGGSRNCIG 11

RESULT 36

US-10-855-532-8

Sequence 8, Application US/10855532
Publication No. US20040259074A1

GENERAL INFORMATION:

APPLICANT: Petkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario

;; COUNTRY: Canada
;; ZIP: M5L 1A9
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
;; COMPUTER: COMPAQ, IBM PC compatible
;; OPERATING SYSTEM: MS-DOS 5.1
;; SOFTWARE: WORD PERFECT
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/855,532
;; FILING DATE: 28-May-2004
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/668,482
;; FILING DATE: 25-Sep-2000
;; APPLICATION NUMBER: 08/882,164
;; FILING DATE: June 25, 1997
;; APPLICATION NUMBER: 08/667,546
;; FILING DATE: June 21, 1996
;; APPLICATION NUMBER: 08/724,466
;; FILING DATE: October 1, 1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hunt, John C.
;; REGISTRATION NUMBER: 36,424
;; REFERENCE/DOCKET NUMBER: 50767/00010
;; TELEPHONE: (416) 863-4344
;; TELEFAX: (416) 863-2653
;;
;; INFORMATION FOR SEQ ID NO: 8
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-10-855-532-8
Query Match 100.0%; Score 33; DB 5; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 2 FSGGARNCIG 11

RESULT 37
US-10-855-532-9
; Sequence 9, Application US/10855532
; Publication No. US20040259074A1
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/855,532
; FILING DATE: 28-May-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,482
; FILING DATE: 25-Sep-2000
; APPLICATION NUMBER: 08/882,164
; FILING DATE: June 25, 1997
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 10
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid

;; APPLICATION NUMBER: 08/667,546
;; FILING DATE: June 21, 1996
;; APPLICATION NUMBER: 08/724,466
;; FILING DATE: October 1, 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hunt, John C.
;; REGISTRATION NUMBER: 36,424
;; REFERENCE/DOCKET NUMBER: 50767/00010
;; TELEPHONE: (416) 863-4344
;; TELEFAX: (416) 863-2653
;;
;; INFORMATION FOR SEQ ID NO: 9
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 9
US-10-855-532-9
Query Match 100.0%; Score 33; DB 5; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 2 FGTGPRNCIG 11

RESULT 38
US-10-855-532-10
; Sequence 10, Application US/10855532
; Publication No. US20040259074A1
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/855,532
; FILING DATE: 28-May-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,482
; FILING DATE: 25-Sep-2000
; APPLICATION NUMBER: 08/882,164
; FILING DATE: June 25, 1997
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 10
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10
US-10-855-532-10

Query Match      100.0%; Score 33; DB 5; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
   |::|::|::|
Db 2 FSGSRNCIG 11

RESULT 39
US-10-021-425-25
; Sequence 25, Application US/10021425
; Publication No. US20030148420A1
; GENERAL INFORMATION:
; APPLICANT: Suzanne L. Bolten
; APPLICANT: Alan M. Easton
; APPLICANT: Leslie C. Engel
; APPLICANT: Dean M. Messing
; APPLICANT: John S. Ng
; APPLICANT: Beverly A. Reitz
; APPLICANT: Scott A. Vaccaro
; APPLICANT: Mark C. Walker
; APPLICANT: Ping T. Wang
; APPLICANT: Robin A. Weinberg
; TITLE OF INVENTION: Aspergillus ochraceus 11 alpha
; FILE REFERENCE: hydroxylase and oxidoreductase
; CURRENT APPLICATION NUMBER: US/10/021,425
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: USSN 60/244,300
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Aspergillus llaoh peptide 3
US-10-021-425-25

Query Match      100.0%; Score 33; DB 4; Length 21;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
   |::|::|::|
Db 4 FGHGVHACPG 13

RESULT 40
US-10-900-856-28
; Sequence 28, Application US/10900856
; Publication No. US2005003473A1
; GENERAL INFORMATION:
; APPLICANT: Bolten, Suzanne L
; APPLICANT: Leslie, Engel C
; APPLICANT: Dean, Messing M
; APPLICANT: John, Ng S
; APPLICANT: Beverly, Reitz A
; APPLICANT: Scott, Vaccaro A
; APPLICANT: Mark, Walker C
; APPLICANT: Ping, Wang T
; APPLICANT: Robin, Weinberg A
; TITLE OF INVENTION: Aspergillus ochraceus 11 alpha hydroxylase and oxidoreductase
; FILE REFERENCE: 3196
; CURRENT APPLICATION NUMBER: US/10/900,856
; CURRENT FILING DATE: 2004-07-28
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patent in version 3.2
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; SEQ ID NO 28
; LENGTH: 21
; TYPE: PRT
; ORGANISM: aspergillus ochraceus llaoh peptide 3
US-10-900-856-28

Query Match      100.0%; Score 33; DB 5; Length 21;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
   |::|::|::|
Db 4 FGHGVHACPG 13

RESULT 41
US-10-103-196-31
; Sequence 31, Application US/10103196
; Publication No. US20030050466A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; FILE REFERENCE: PT008P1
; CURRENT APPLICATION NUMBER: US/10/103,196
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/707,936
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/13504
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 60/178,770
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/149,447
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/138,573
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 60/137,797
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/135,122
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-196-31

Query Match      100.0%; Score 33; DB 4; Length 23;
Best Local Similarity 40.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
   |::|::|::|
Db 5 FLGLGLGCCG 14

RESULT 42
US-09-749-637A-126
; Sequence 126, Application US/09749637A
; Patent No. US20020173449A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
```

; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 126
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus marmoreus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(30)
; OTHER INFORMATION: Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 28 may be Trp or bromo-Trp
; OTHER INFORMATION: s 24 and 28 may be Trp or bromo-Trp
US-09-749-637A-126

Query Match 100.0%; Score 33; DB 3; Length 30;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|||:|
Db 14 FKIGXCCSG 23

RESULT 43
US-09-749-637A-129
; Sequence 129, Application US/09749637A
; Patent No. US20020173449A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren
; APPLICANT: Hilliard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 129
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus striatus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(30)
; OTHER INFORMATION: Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 28 may be Trp or bromo-Trp
; OTHER INFORMATION: s 24 and 28 may be Trp or bromo-Trp
US-09-749-637A-129

Query Match 100.0%; Score 33; DB 3; Length 30;

Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGXGXXCXG 10
|::|||:|
Db 14 FKIGXCCSG 23

RESULT 44
US-09-749-637A-283
; Sequence 283, Application US/09749637A
; Patent No. US20020173449A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren
; APPLICANT: Hilliard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 283
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus geographus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(30)
; OTHER INFORMATION: Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 28 may be Trp or bromo-Trp
; OTHER INFORMATION: s 24 and 28 may be Trp or bromo-Trp
US-09-749-637A-283

Query Match 100.0%; Score 33; DB 3; Length 30;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|||:|
Db 14 FKIGXCCSG 23

RESULT 45
US-10-433-485A-1
; Sequence 1, Application US/10433485A
; Publication No. US20040131617A1
; GENERAL INFORMATION:
; APPLICANT: WHITE, Jay A.
; APPLICANT: PETKOVICH, P. Martin
; APPLICANT: JONES, Glenville
; APPLICANT: RAMSHAW, Heather
; TITLE OF INVENTION: P45ORAI-2(P450 Cytochrome 26B), Encoding Nucleic Acid
; FILE REFERENCE: 11812-78
; CURRENT APPLICATION NUMBER: US/10/433,485A
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: PCT/CA01/01805
; PRIOR FILING DATE: 2001-12-17

;; PRIOR APPLICATION NUMBER: PCT/CA00/01493
;; PRIOR FILING DATE: 2000-12-15
;; PRIOR APPLICATION NUMBER: 60/178,314
;; PRIOR FILING DATE: 2000-01-27
;; PRIOR APPLICATION NUMBER: 60/171,110
;; PRIOR FILING DATE: 1999-12-16
;; NUMBER OF SEQ ID NOS: 48
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 1
;; LENGTH: 30
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: typical heme binding motif found in all Cytochrome P450s
US-10-433-485A-1

Query Match 100.0%; Score 33; DB 4; Length 30;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 8 FGIGKRVCMG 17

RESULT 46
US-10-839-227-126
;; Sequence 126, Application US/10839227
;; Publication No. US20050214903A1
;; GENERAL INFORMATION:
;; APPLICANT: University of Utah Research Foundation
;; APPLICANT: Cognetix, Inc.
;; APPLICANT: Olivera, Baldomero M.
;; APPLICANT: Cartier, G. Edward
;; APPLICANT: Watkins, Maren
;; APPLICANT: Hillyard, David R.
;; APPLICANT: McIntosh, J. Michael
;; APPLICANT: Layer, Richard T.
;; APPLICANT: Jones, Robert M.
;; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
;; FILE REFERENCE: 2314-277
;; CURRENT APPLICATION NUMBER: US/10/839,227
;; CURRENT FILING DATE: 2004-05-06
;; PRIOR FILING DATE: 2000-12-28
;; PRIOR APPLICATION NUMBER: US 60/243,412
;; PRIOR FILING DATE: 2000-10-27
;; PRIOR APPLICATION NUMBER: US60/219,440
;; PRIOR FILING DATE: 2000-07-20
;; PRIOR FILING DATE: 2000-06-26
;; PRIOR FILING DATE: 1999-12-30
;; NUMBER OF SEQ ID NOS: 409
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 126
;; LENGTH: 30
;; TYPE: PRT
;; ORGANISM: Conus marmoreus
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (1)...(30)
;; OTHER INFORMATION: Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r

;; OTHER INFORMATION: esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue
;; OTHER INFORMATION: s 24 and 28 may be Trp or bromo-Trp
US-10-839-227-126
Query Match 100.0%; Score 33; DB 5; Length 30;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXXGXXXCXG 10
|::|::|::|::|
Db 8 FGIGKRVCMG 17

US-10-839-227-126
Query Match 100.0%; Score 33; DB 5; Length 30;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXXGXXXCXG 10
|::|::|::|::|

Db 14 FKIGXXCCSG 23
RESULT 47
US-10-839-227-129
;; Sequence 129, Application US/10839227
;; Publication No. US20050214903A1
;; GENERAL INFORMATION:
;; APPLICANT: University of Utah Research Foundation
;; APPLICANT: Cognetix, Inc.
;; APPLICANT: Olivera, Baldomero M.
;; APPLICANT: Cartier, G. Edward
;; APPLICANT: Watkins, Maren
;; APPLICANT: Hillyard, David R.
;; APPLICANT: McIntosh, J. Michael
;; APPLICANT: Layer, Richard T.
;; APPLICANT: Jones, Robert M.
;; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
;; FILE REFERENCE: 2314-277
;; CURRENT APPLICATION NUMBER: US/10/839,227
;; CURRENT FILING DATE: 2004-05-06
;; PRIOR FILING DATE: 2000-12-28
;; PRIOR APPLICATION NUMBER: US 60/243,412
;; PRIOR FILING DATE: 2000-10-27
;; PRIOR APPLICATION NUMBER: US60/219,440
;; PRIOR FILING DATE: 2000-07-20
;; PRIOR FILING DATE: 2000-06-26
;; PRIOR FILING DATE: 1999-12-30
;; NUMBER OF SEQ ID NOS: 409
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 129
;; LENGTH: 30
;; TYPE: PRT
;; ORGANISM: Conus striatus
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (1)...(30)
;; OTHER INFORMATION: Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r
;; OTHER INFORMATION: esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue
;; OTHER INFORMATION: s 24 and 28 may be Trp or bromo-Trp
US-10-839-227-129
Query Match 100.0%; Score 33; DB 5; Length 30;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXXGXXXCXG 10
|::|::|::|::|
Db 14 FKIGXXCCSG 23
RESULT 48
US-10-839-227-283
;; Sequence 283, Application US/10839227
;; Publication No. US20050214903A1
;; GENERAL INFORMATION:
;; APPLICANT: University of Utah Research Foundation
;; APPLICANT: Cognetix, Inc.
;; APPLICANT: Olivera, Baldomero M.
;; APPLICANT: Cartier, G. Edward
;; APPLICANT: Watkins, Maren
;; APPLICANT: Hillyard, David R.
;; APPLICANT: McIntosh, J. Michael
;; APPLICANT: Layer, Richard T.
;; APPLICANT: Jones, Robert M.
;; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
;; FILE REFERENCE: 2314-277
;; CURRENT APPLICATION NUMBER: US/10/839,227
;; CURRENT FILING DATE: 2004-05-06
;; PRIOR FILING DATE: 2004-05-06
;; PRIOR APPLICATION NUMBER: US 09/749,637

; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 283
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus geographus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(30)
; OTHER INFORMATION: Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at re
; OTHER INFORMATION: sidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues
; OTHER INFORMATION: 24 and 28 may be Trp or bromo-Trp
US-10-839-227-283

Query Match 100.0%; Score 33; DB 5; Length 30;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 14 FKIGXCXCSG 23

RESULT 49

US-10-437-963-159510
; Sequence 159510, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 159510
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_5887C.1.pep
US-10-437-963-159510

Query Match 100.0%; Score 33; DB 4; Length 32;
Best Local Similarity 40.0%; Pred. No. 1e+03;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 5 FIGIWSCEG 14

RESULT 50

US-10-351-641-487
; Sequence 487, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:

; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 487
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-487

Query Match 100.0%; Score 33; DB 4; Length 35;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 26 FLGGTVCLG 35

Search completed: March 8, 2006, 11:28:19
Job time : 167 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 8, 2006, 11:16:36 ; Search time 189 Seconds
(without alignments)
23.248 Million cell updates/sec

Title: US-10-751-235-14
Perfect score: 33
Sequence: 1 FXGXGXXCXG 10

Scoring table: *BLOSUM62DX - two matrix follows an Xae in the query seq to match anything in the database sequence.*

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

2443163 These matches

are counted as

conservative substitutions

in the alignment &

are marked with a

colon (:).

50 alignments saved

as requested

Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	10	2	AAY09193
2	33	100.0	10	3	AAY91408
3	33	100.0	10	4	AAI10370
4	33	100.0	10	4	AAI10370
5	33	100.0	10	4	AAI10370
6	33	100.0	10	4	AAI10370
7	33	100.0	10	5	AAI10370
8	33	100.0	10	5	AAI10370
9	33	100.0	10	5	AAI10370
10	33	100.0	10	6	AAI10370
11	33	100.0	10	6	AAI10370
12	33	100.0	10	6	AAI10370
13	33	100.0	10	6	AAI10370
14	33	100.0	10	7	AAI10370
15	33	100.0	10	7	AAI10370
16	33	100.0	10	9	AAI10370
17	33	100.0	10	9	AAI10370
18	33	100.0	10	11	AAI10370
19	33	100.0	10	11	AAI10370
20	33	100.0	10	11	AAI10370
21	33	100.0	10	11	AAI10370
22	33	100.0	10	11	AAI10370
23	33	100.0	10	11	AAI10370
24	33	100.0	10	11	AAI10370

25	33	100.0	11	2	AA41632
26	33	100.0	11	2	AA41633
27	33	100.0	11	2	AA40873
28	33	100.0	11	2	AA40878
29	33	100.0	11	2	AA40880
30	33	100.0	11	2	AA40870
31	33	100.0	11	2	AA40871
32	33	100.0	11	2	AA41635
33	33	100.0	11	2	AA40875
34	33	100.0	11	5	AAU80018
35	33	100.0	11	5	AD058606
36	33	100.0	11	6	AAE30014
37	33	100.0	13	2	AA30868
38	33	100.0	13	2	AAU09192
39	33	100.0	13	3	AAE11394
40	33	100.0	14	4	AG98132
41	33	100.0	15	1	AA20076
42	33	100.0	15	1	AAE50146
43	33	100.0	15	1	AAE60758
44	33	100.0	15	1	AA24422
45	33	100.0	15	2	AA82090
46	33	100.0	15	3	AAE19305
47	33	100.0	15	5	AAU91319
48	33	100.0	15	6	ABG75617
49	33	100.0	15	6	ABG75617
50	33	100.0	15	9	ADV23625
51	33	100.0	15	9	ADV23253
52	33	100.0	16	2	AA38307
53	33	100.0	16	3	AAE5096
54	33	100.0	16	6	ABJ26710
55	33	100.0	16	8	ADU72660
56	33	100.0	16	9	ADZ73651
57	33	100.0	18	2	AAW15123
58	33	100.0	20	2	AAV13668
59	33	100.0	20	2	AAW26982
60	33	100.0	20	4	AAU05333
61	33	100.0	20	5	ABU09980
62	33	100.0	20	5	AAE15327
63	33	100.0	20	7	ADM34802
64	33	100.0	20	7	ADM33569
65	33	100.0	20	7	ADM36246
66	33	100.0	20	8	ADU66830
67	33	100.0	20	8	ADU66828
68	33	100.0	20	8	ADU66829
69	33	100.0	20	8	ADU66831
70	33	100.0	20	8	ADU66827
71	33	100.0	20	9	ADU90770
72	33	100.0	20	9	ADU90768
73	33	100.0	20	9	ADU90767
74	33	100.0	20	9	ADU90771
75	33	100.0	20	9	ADU90769
76	33	100.0	20	9	ADY62584
77	33	100.0	20	9	ADY62585
78	33	100.0	20	9	ADY62587
79	33	100.0	20	9	ADY62588
80	33	100.0	20	9	ADY62586
81	33	100.0	21	5	AAE25786
82	33	100.0	22	4	AAE87046
83	33	100.0	23	4	AAE87038
84	33	100.0	23	4	AAE49519
85	33	100.0	23	4	AAU05872
86	33	100.0	30	4	AAU05874
87	33	100.0	30	4	AAU05978
88	33	100.0	30	4	AAE85150
89	33	100.0	30	5	ABE52141
90	33	100.0	33	8	ADL97623
91	33	100.0	34	8	ADM78246
92	33	100.0	34	8	ADM78312
93	33	100.0	34	8	ADM78221
94	33	100.0	34	8	ADM78254
95	33	100.0	35	3	AAE89167
96	33	100.0	35	3	AAE89126
97	33	100.0	35	3	AAE89164

98 33 100.0 35 3 AAY89129 Core poly
99 33 100.0 35 3 AAY89127 Core poly
100 33 100.0 35 3 AAY89163 Core poly

ALIGNMENTS

RESULT 1
ID AAY09193 standard; peptide; 10 AA.

AC AAY09193;

DT 20-JUL-1999 (first entry)

XX Soybean cytochrome P450 enzyme conserved peptide motif.

XX Soybean; Solanaceae crop plant; cytochrome P450; transgenic plant;
KW enzyme; phenylurea herbicide; herbicide resistance.

XX Glycine max.

OS Key Location/Qualifiers

FT Misc-difference 1..10

FT /note= "Xaa is any amino acid"

XX WO9919493-A2.

XX 22-APR-1999.

XX 05-OCT-1998; 98WO-US020807.

XX 10-OCT-1997; 97US-00948564.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Siminszky B, Dewey RE, Corbin FT;

XX WPI; 1999-302532/25.

XX DNA encoding soybean cytochrome P450 enzymes.

XX Example 2; Page 26; 93pp; English.

XX The invention provides new DNA molecules (AAX60773-X60781) encoding
CC soybean cytochrome P450 enzymes (AAY09183-Y09191) respectively. The DNA
CC encoding the cytochrome P450 enzymes is useful for transformation of
CC Solanaceae crop plants. Transgenic plants comprising DNA constructs
CC having the P450 encoding nucleic acid sequences are resistant to
CC phenylurea herbicides. The transgenic plants have increased resistance to
CC The plant crops, e.g. turfgrass, tobacco, potato, corn, rice,
CC cotton, soybean, rape, wheat, oats, barley or rice are particularly
CC resistant to fluometuron, linuron, chlortoluron or diuron

XX Sequence 10 AA;

Query Match 100.0%; Score 33; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXCXG 10

Db 1 FXXGXXCXG 10

RESULT 2

AA91408

ID AAY91408 standard; protein; 10 AA.

XX AC AAY91408;

XX

29-JUN-2000 (first entry)

Human secreted protein sequence encoded by gene 3 SEQ ID NO:129.

Human; secreted protein; diagnosis; neuroprotective; neurotropic;
KW neuroleptic; antimanic; cerebroprotective; immunomodulatory;
KW anti-microbial; cardiant; cytostatic; antiinflammatory; haemostatic;
KW anticonvulsant; vasotropic; vaccine; gene therapy; anti-sense therapy;
KW neural; reproductive; immune disorder; immunodeficiency; infection;
KW lymphoma; demyelinating disease; autoimmunity; cancer; inflammation;
KW aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; Tourette syndrome; multiple sclerosis; meningitis;
KW ischaemia; mania; dementia; obsessive compulsive disorder;
KW viral prophylaxis; developmental disorder; sexually-linked disorder;
KW cardiovascular disorder; food additive; preservative; chromosome 11.

XX Homo sapiens.

XX WO200011014-A1.

XX 02-MAR-2000.

XX 24-AUG-1999; 99WO-US019330.

XX 25-AUG-1998; 98US-0097917P.

XX 31-AUG-1998; 98US-0098634P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Moore PA, Ruben SM, Olsen HS, Shi Y, Rosen CA, Florence KA;
PI Soppet DR, Lafleur DW, Endress GA, Ebner R, Komatsoulis G, Duan RD;
PI WPI; 2000-224656/19.

XX Novel secreted proteins and corresponding DNA molecules that can be used
XX to prevent, treat and diagnose disease in humans, for example,
XX Alzheimer's, cancer, and immune disorders.

XX Disclosure; Page 390; 416pp; English.

XX The polynucleotide sequences given in AAA26281 to AAA26336 encode the
CC human secreted proteins given in AAY91346 to AAY91449. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: neuroprotective; neurotropic;
CC neuroleptic; antimanic; cerebroprotective; immunomodulatory; anti-
CC microbial; cardiant; cytostatic; antiinflammatory; haemostatic;
CC anticonvulsant; and vasotropic. The polynucleotides and proteins may be
CC used to prevent, treat or ameliorate a medical condition, e.g. by protein
CC or gene therapy. Conditions treatable by the proteins of the invention
CC include neural, reproductive, or immune disorders, especially
CC immunodeficiency, infection, lymphomas, demyelinating diseases, auto-
CC immunities, cancer, general microbial infection, inflammation, aneurysms
CC and haemorrhages. Specific examples include: Alzheimer's disease;
CC Parkinson's; Huntington's; Tourette syndrome; multiple sclerosis;
CC meningitis; ischaemia; prostate cancer; mania; dementia; obsessive
CC compulsive disorder and viral prophylaxis. The polynucleotides and
CC proteins can also be used in the detection of disorders associated with
CC the function of the protein, for example, the detection of developmental
CC disorders, sexually-linked disorders, or disorders of the cardiovascular
CC system. They may also be used as food additives or preservatives.
CC AAA26272 to AAA26280 and AAY91345 are sequences used in the
CC exemplification of the present invention

XX Sequence 10 AA;

Query Match 100.0%; Score 33; DB 3; Length 10;

Best Local Similarity 40.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXCXG 10

Db 1 FSLGRRHCLG 10

RESULT 5
AA09243
ID AAM09243 standard; peptide; 10 AA.
XX AC AAM09243;
XX DT 09-OCT-2001 (first entry)
XX DE HLA-A1 decamer #110.
XX KW Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
XX KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
XX KW major histocompatibility complex; antigen presenting cell; melanoma;
XX KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
XX OS Homo sapiens.
XX PN WO200135810-A2.
XX PD 25-MAY-2001.
XX PF 15-NOV-2000; 2000WO-US031513.
XX PR 15-NOV-1999; 99US-0165590P.
XX PA (DAND) DANA FARBER CANCER INST INC.
XX PA (UYBO-) UNIV BOSTON.
XX PI Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
XX PI Von Bergwelt- Baildon M;
XX PI WPI; 2001-355537/37.
XX DR
XX PT Treating a cancer patient involves administering to patient a cytotoxic T
XX PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide
XX PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.
XX PS Disclosure; Page 70; 121pp; English.
XX CC The present invention describes a method for treating a patient having,
XX CC or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),
XX CC which involves administering to the patient a cytotoxic T-lymphocyte
XX CC (CTL) that kills the cell, an antigen presenting cell (APC) that
XX CC activates CTL, a peptide of CYP1B1 that binds to major histocompatibility
XX CC complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or
XX CC peptide of CYP1B1. Also described are: (1) a method for assessing the
XX CC level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that
XX CC binds to MHC complex molecule, involving measuring the level of CTL
XX CC specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient
XX CC ; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex
XX CC vivo generated CTL (II) that specifically kills a cell expressing CYP1B1
XX CC in a specific of a MHC complex-restricted fashion; and (4) an ex vivo
XX CC generated APC (III) that presents a peptide of a CYP1B1 in the context of
XX CC a MHC complex molecule. The method is useful for treating a patient
XX CC having or is at risk of having a cell that expresses CYP1B1. The method
XX CC is useful for the prevention, treatment and diagnosis of cancer, e.g.
XX CC melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and
XX CC lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and
XX CC brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can
XX CC bind to human leukocyte antigens (HLAs), as well as other amino acid
XX CC sequence used in the exemplification of the present invention
XX SQ Sequence 10 AA;
Query Match 100.0%; Score 33; DB 4; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 1 FSVGKRCIG 10

RESULT 6
AAM10626
ID AAM10626 standard; peptide; 10 AA.
XX AC AAM10626;
XX DT 09-OCT-2001 (first entry)
XX DE HLA-A *0201 decamer #409.
XX KW Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
XX KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
XX KW major histocompatibility complex; antigen presenting cell; melanoma;
XX KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
XX OS Homo sapiens.
XX PN WO200135810-A2.
XX PD 25-MAY-2001.
XX PF 15-NOV-2000; 2000WO-US031513.
XX PR 15-NOV-1999; 99US-0165590P.
XX PA (DAND) DANA FARBER CANCER INST INC.
XX PA (UYBO-) UNIV BOSTON.
XX PI Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
XX PI Von Bergwelt- Baildon M;
XX PI WPI; 2001-355537/37.
XX DR
XX PT Treating a cancer patient involves administering to patient a cytotoxic T
XX PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide
XX PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.
XX PS Disclosure; Page 78; 121pp; English.
XX CC The present invention describes a method for treating a patient having,
XX CC or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),
XX CC which involves administering to the patient a cytotoxic T-lymphocyte
XX CC (CTL) that kills the cell, an antigen presenting cell (APC) that
XX CC activates CTL, a peptide of CYP1B1 that binds to major histocompatibility
XX CC complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or
XX CC peptide of CYP1B1. Also described are: (1) a method for assessing the
XX CC level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that
XX CC binds to MHC complex molecule, involving measuring the level of CTL
XX CC specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient
XX CC ; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex
XX CC vivo generated CTL (II) that specifically kills a cell expressing CYP1B1
XX CC in a specific of a MHC complex-restricted fashion; and (4) an ex vivo
XX CC generated APC (III) that presents a peptide of a CYP1B1 in the context of
XX CC a MHC complex molecule. The method is useful for treating a patient
XX CC having or is at risk of having a cell that expresses CYP1B1. The method
XX CC is useful for the prevention, treatment and diagnosis of cancer, e.g.
XX CC melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and
XX CC lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and
XX CC brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can
XX CC bind to human leukocyte antigens (HLAs), as well as other amino acid
XX CC sequence used in the exemplification of the present invention
XX SQ Sequence 10 AA;
Query Match 100.0%; Score 33; DB 4; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 1 FSVGKRCIG 10

CC hypercalcaemia, malabsorption syndrome, steatorrhoea, and tropical sprue;
 CC or cholesterol, steroid and other lipid metabolic disorders. The present
 CC sequence represents a conserved haem region generic peptide, which is
 CC used in an example from the present invention
 XX
 QQ Sequence 10 AA;

Query Match 100.0%; Score 33; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e-02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
 Db 1 ||||| 10
 1 FXXGXXXCXG 10

RESULT 8
 ABP53085
 ID ABP53085 standard; peptide; 10 AA.
 XX
 AC ABP53085;
 XX
 DT 11-NOV-2002 (first entry)
 XX
 DE CYP 27C1 haem-binding signature peptide SEQ ID NO:47.
 XX
 KW Cloning; Characterisation; human; cytochrome P450; CYP 27C1; cytosstatic;
 KW thromimetic; antidiabetic; antipsoriatic; tuberculostatic; osteopathic;
 KW dermatological; antilipemic; gene therapy; vaccine; Vitamin D; diabetes;
 KW vitamin D metabolic deficiency; hyperparathyroidism; hypoparathyroidism;
 KW medullary carcinoma; psoriasis; sarcoidosis; tuberculosis; osteomalacia;
 KW chronic renal disease; vitamin D dependent rickets; anticonvulsant;
 KW fibrogenesis imperfecta ossium; osteitis fibrosa cystica; osteoporosis;
 KW osteopenia; osteosclerosis; renal osteodystrophy; rickets; steatorrhoea;
 KW glucocorticoid antagonism; idiopathic hypercalcaemia; tropical sprue;
 KW malabsorption syndrome; cholesterol steroid; lipid metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 XX W0200264765-A2.
 XX
 XX 22-AUG-2002.
 XX
 XX 11-FEB-2002; 2002WO-CA000163.
 XX
 XX 09-FEB-2001; 2001US-0267410P.
 XX
 XX (CYTO-) CYTOCHROME INC.
 XX
 XX Wisniewski J;
 XX
 XX WPI; 2002-657595/70.
 XX
 XX New nucleic acid molecules encoding cytochrome P450 proteins, human CYP
 XX 27C1 and a hybrid homologs from *Xenopus laevis*, useful for treating
 XX diseases related to vitamin D or vitamin D metabolite deficiency, e.g.
 XX parathyroidism and diabetes.

Example 1; Page 16; 209pp; English.

The present invention describes an isolated nucleic acid molecule (I)
 encoding human cytochrome P450, CYP 27C1, and a hybrid homologue from
Xenopus laevis. (I) has thymimetic, antidiabetic, cytosstatic,
 antipsoriatic, tuberculostatic, osteopathic, dermatological and
 antilipemic activities, and can be used in gene therapy and in vaccines.
 The nucleic acid molecules, proteins and methods from the present
 invention are useful for treating diseases related to vitamin D or
 vitamin D metabolite deficiency, e.g. hyper- and hypo-parathyroidism,
 Oseudohypo-parathyroidism, Secondary hyperparathyroidism, diabetes,
 medullary carcinoma, psoriasis, sarcoidosis, tuberculosis, chronic renal
 disease, hypophosphatemic VNR, vitamin D dependent rickets,
 anticonvulsant treatment, fibrogenesis imperfecta ossium, osteitis
 fibrosa cystica, osteomalacia, osteoporosis, osteopenia, osteosclerosis,
 CC

RESULT 7	
ABP53084	
ID	ABP53084 standard; peptide; 10 AA.
XX	
AC	ABP53084;
XX	
DT	11-NOV-2002 (first entry)
XX	
DE	Conserved haem region generic peptide.
XX	
KW	Cloning; characterisation; human; cytochrome P450; CYP 27C1; cytostatic;
KW	thyromimetic; antidiabetic; antipsoriatic; tuberculostatic; osteopathic;
KW	dermatological; antilipemic; gene therapy; vaccine; vitamin D; diabetes;
KW	vitamin D metabolite deficiency; hyperparathyroidism; hypoparathyroidism;
KW	medullary carcinoma; psoriasis; sarcoidosis; tuberculosis; osteomalacia;
KW	chronic renal disease; vitamin D dependent rickets; anticonvulsant;
KW	fibrogenesis imperfecta ossium; osteitis fibrosa cystica; osteoporosis;
KW	osteopaenia; osteosclerosis; renal osteodystrophy; rickets; steatorrhea;
KW	glucocorticoid antagonism; idiopathic hypercalcaemia; tropical sprue;
KW	malabsorption syndrome; cholesterol steroid; lipid metabolic disorder.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 2
FT	/note= "unspecified"
FT	Misc-difference 3
FT	/note= "unspecified"
FT	Misc-difference 5
FT	/note= "unspecified"
FT	Misc-difference 6
FT	/note= "unspecified"
FT	Misc-difference 7
FT	/note= "unspecified"
FT	Misc-difference 9
FT	/note= "unspecified"
XX	
PN	WO200264765-A2.
XX	
PD	22-AUG-2002.
XX	
PF	11-FEB-2002; 2002WO-CA000163.
XX	
PR	09-FEB-2001; 2001US-0267410P.
XX	
PA	(CYTO-) CYTOCHROME INC.
XX	
PI	Wisniewski J;
XX	
DR	WPI; 2002-657595/70.
XX	
PT	New nucleic acid molecules encoding cytochrome P450 proteins, human CYP
PT	27C1 and a hybrid homologs from Xenopus laevis, useful for treating
PT	diseases related to vitamin D or vitamin D metabolite deficiency, e.g.
PT	parathyroidism and diabetes.
XX	
PS	Example 1; Page 86; 209pp; English.
XX	
CC	The present invention describes an isolated nucleic acid molecule (I)
CC	encoding human cytochrome P450, CYP 27C1, and a hybrid homologue from
CC	Xenopus laevis. (I) has thyromimetic, antidiabetic, cytostatic,
CC	antipsoriatic, tuberculostatic, osteopathic, dermatological and
CC	antilipemic activities, and can be used in gene therapy and in vaccines.
CC	The nucleic acid molecules, proteins and methods from the present
CC	invention are useful for treating diseases related to vitamin D or
CC	vitamin D metabolite deficiency, e.g. hyper- and hypo-parathyroidism,
CC	Oxodihydro-parathyroidism, Secondary hyperparathyroidism, diabetes,
CC	medullary carcinoma, psoriasis, sarcoidosis, tuberculosis, chronic renal
CC	disease, hypophosphatemic VDDR, vitamin D dependent rickets,
CC	anticonvulsant treatment, fibrogenesis imperfecta ossium, osteitis
CC	fibrosa cystica, osteomalacia, osteoporosis, osteopaenia, osteosclerosis,
CC	renal osteodystrophy, rickets, glucocorticoid antagonism, idiopathic

CC renal osteodystrophy, rickets, glucocorticoid antagonism, idiopathic
 CC hypercalcaemia, malabsorption syndrome, steatorrhoea, and tropical sprue,
 CC or cholesterol, steroid and other lipid metabolic disorders. The present
 CC sequence represents a CYP 27C1 haem-binding signature peptide, which is
 CC used in an example from the present invention

XX Sequence 10 AA;

Query Match 100.0%; Score 33; DB 5; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
 |::|::|::|
 Db 1 FGHGVRSCIG 10

RESULT 9

AAE25791
 ID AAE25791 standard; peptide; 10 AA.

XX AC AAE25791;

XX DT 04-NOV-2002 (first entry)

XX DE Aspergillus ochraceus cytochrome p450 conserved haem binding motif.

XX KW 11 alpha hydroxylase; enzyme; sitosterol; eplerenone; cell therapy;
 XX KW steroid bioconversion; antiinflammatory; antiarthritic; cytostatic;
 XX KW cardiant; cytochrome P450; oxidoreductase; haem binding motif.

XX OS Aspergillus ochraceus.

XX FH Key Location/Qualifiers

XX FT Misc-difference 2. .3

XX FT /label= Unknown

XX FT Misc-difference 5. .7

XX FT /label= Unknown

XX FT Misc-difference 9

XX FT /label= Unknown

XX PN WO200246386-A2.

XX PD 13-JUN-2002.

XX PF 26-OCT-2001; 2001WO-US051070.

XX PR 30-OCT-2000; 2000US-0244300P.

XX PA (PHAA) PHARMACIA CORP.

XX PA (BOLT/) BOLTON S.

XX PA (CLAY/) CLAYTON R.

XX PA (EAST/) EASTON A.

XX PA (ENGE/) ENGEL L.

XX PA (MESS/) MESSING D.

XX XX Bolton S, Clayton R, Easton A, Engel L, Messing D;

XX PI WPI; 2002-547772/58.

XX DR New isolated Aspergillus ochraceus 11 alpha-hydroxylase or

XX FT oxidoreductase, for bioconversion of steroid substances to their 11 alpha

XX FT hydroxy counterparts in heterologous cells.

XX PS Example 10; Page 57; 181pp; English.

XX CC The present invention relates to novel cytochrome p450-like enzyme

XX CC (Aspergillus ochraceus 11 alpha hydroxylase protein), oxidoreductases and

XX CC polynucleotides encoding such proteins. Host cells comprising the

XX CC sequences of the invention are useful for making one or more enzymes from

XX CC the metabolic pathway for the synthesis of sitosterol to eplerenone. They

XX CC are useful for selective oxidation of a compound to an hydroxylated

XX CC product. Compositions of the invention are useful for producing spores

CC from A. ochraceus, A. niger, A. nidulans, Rhizopus oryzae, R. stolonifer,
 CC R. arrhizus Trichothecium roseum, Fusarium oxysporum and M. olivaceum
 CC etc, preferably to produce spores from A. ochraceus. Sequences of the
 CC invention are useful in bioconversion of steroid substances to their 11
 CC alpha-hydroxy counterparts. They are also used in cell therapy. The
 CC present sequence is A. ochraceus cytochrome p450 conserved haem binding
 CC motif

XX Sequence 10 AA;

Query Match 100.0%; Score 33; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
 |::|::|::|
 Db 1 FXXGXXXCXG 10

RESULT 10

ABU08352
 ID ABU08352 standard; peptide; 10 AA.

XX AC ABU08352;

XX DT 30-MAY-2003 (first entry)

XX DE Conserved haem-binding motif found in eukaryotic P450 monooxygenases.

XX KW Cytochrome P450; (+)-delta-cadinene 8-hydroxylase; CYP706B1;

XX KW biosynthesis of gossypol; sesquiterpene; cotton seed; cotton cultivate;

XX KW sesquiterpenoid; livestock feed; monooxygenase; haem-binding motif.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 2. .3

XX FT /note= "Any amino acid"

XX FT Misc-difference 5

XX FT /note= "Any amino acid"

XX FT Misc-difference 7

XX FT /note= "Any amino acid"

XX FT Misc-difference 9

XX FT /note= "Any amino acid"

XX PN US2002187538-A1.

XX PD 12-DEC-2002.

XX PF 07-FEB-2002; 2002US-00067534.

XX PR 07-FEB-2001; 2001US-0267160P.

XX PA (ESSE/) ESSENBERG M K.

XX PA (CHEN/) CHEN X.

XX PA (LUOP/) LUO P.

XX PA (WANG/) WANG Y.

XX XX Essenberg MK, Chen X, Luo P, Wang Y;

XX PI WPI; 2003-341036/32.

XX DR Novel cotton (+)-gamma-cadinene 8-hydroxylase polypeptide designated as

XX FT CYP706B1, useful as target for suppression of biosynthesis of gossypol

XX FT formation in cotton seeds.

XX PS Example 1; Page 6; 26pp; English.

XX CC The present invention relates to the isolation of cotton (+)-delta-

XX CC cadinene 8-hydroxylase (designated as CYP706B1), and the polynucleotide

XX CC sequence encoding it. The CYP706B1 protein is a cytochrome P450 which is

XX CC useful as a target for suppression of the biosynthesis of gossypol and

XX CC related sesquiterpenes in cotton seeds through genetic engineering

CC techniques. The polynucleotide sequence encoding CYP706B1 is useful in
 CC suppression of the biosynthesis of gossypol and related sesquiterpenes in
 CC cotton seeds, where the polynucleotide sequence is expressed in antisense
 CC or sense orientation as a perfect match to the native gene whose
 CC expression is sought to be suppressed. The polynucleotide sequence of the
 CC invention is useful for producing cotton cultivars which avoid the
 CC presence of sesquiterpenoids in their seeds, and for producing cotton
 CC seed product which is suitable for use as a feed for both livestock and
 CC humans. The present sequence represents a highly conserved haem-binding
 CC motif found in eukaryotic P450 monooxygenases

SQ Sequence 10 AA;

Query Match 100.0%; Score 33; DB 6; Length 10;
 Best Local Similarity 90.0%; Pred. No. 3.5e+02;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXCXG 10

Db 1 FXGXXXXCXG 10

RESULT 11

ABR42010
 ID ABR42010 standard; peptide; 10 AA.

XX AC ABR42010;

DT 11-AUG-2003 (first entry)

DE Cytochrome P450 conserved motif.

XX Cytochrome P450; EthB; ether; ethyl tert-butyl ether; ETBE; degradation;
 KW bioremediation; soil decontamination; pollutant; biosensor;
 KW Rhodococcus ruber.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 3 /note= "any amino acid"

FT Misc-difference 5 /note= "any amino acid"

FT Misc-difference 7 /note= "any amino acid"

FT Misc-difference 9 /note= "any amino acid"

FT Misc-difference 9 /note= "any amino acid"

XX EPI270722-A1.

XX 02-JAN-2003.

XX 22-JUN-2001; 2001EP-00401667.

XX 22-JUN-2001; 2001EP-00401667.

XX (INSP) INST PASTEUR.

XX (INSP) INST FRANCAIS DU PETROLE.

XX Chauvaux S, Miras I, Beguin P;

XX WPI; 2003-334761/32.

XX New Rhodococcus ruber nucleic acid, useful for transforming bacteria for
 PT depolluting soil contaminated with ethyl tert-butyl ether comprises the
 PT cytochrome P-450 gene cluster involved in cleavage of ethyl tert-butyl
 PT ether.

XX Example 5; Page 10; 58pp; English.

XX The present sequence is a consensus motif of cytochrome P450s, and
 CC includes a Cys residue that is strictly conserved in all cytochrome
 CC P450s. The motif has been identified in the EthB protein (see ABR42001)

CC of Rhodococcus ruber strain CNCM I-1899 cells. EthB is an ethyl tert-
 CC butyl ether (ETBE)-induced cytochrome P450. It forms part of a cytochrome
 CC P450 system involved in the cleavage of ether fuel additives. Recombinant
 CC host cells comprising a vector encoding eth genes, and which are capable
 CC of ETBE degradation or mineralization, can be used for bioremediation of
 CC a contaminated soil or effluent

SQ Sequence 10 AA;

Query Match 100.0%; Score 33; DB 6; Length 10;

Best Local Similarity 80.0%; Pred. No. 3.5e+02;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXCXG 10

Db 1 FXGXXXXCXG 10

RESULT 12

AAE35263

ID AAE35263 standard; peptide; 10 AA.

XX AC AAE35263;

XX 28-MAY-2003 (first entry)

DE Cytochrome P450 putative family signature peptide #2.

XX Human; retinoic acid; vitamin A; cytochrome P450; actinic keratosis;
 KW P450RAI; cancer; psoriasis; acne; ichthyosis; gene therapy; vaccine;
 KW enzyme.

XX Unidentified.

XX WO200295034-A2.

XX 28-NOV-2002.

XX 23-MAY-2002; 2002WO-CA000758.

XX 23-MAY-2001; 2001US-0292531P.

XX (CYTO-) CYTOCHROMA INC.

XX Wisniewski J, Petkovich PM, Ramshaw H;

XX WPI; 2003-112152/10.

XX New isolated P450RAI-3 nucleic acid molecule and polypeptide, useful for
 PT diagnosing, preventing, or treating disorders with aberrant expression or
 PT activity of the P450RAI-3, such as cancer, actinic keratosis, acne and
 PT psoriasis.

XX Example 1; Page 72; 231pp; English.

XX The invention relates to retinoic acid metabolising cytochrome P450,
 CC P450RAI polypeptides and polynucleotides. Methods and compositions of the
 CC invention are useful for diagnosing, preventing, ameliorating and/or
 CC treating disorders associated with the aberrant expression or activity of
 CC the P450RAI such as diseases related to vitamin A and retinoic acid
 CC metabolism, e.g. cancer, actinic keratosis, psoriasis, acne and
 CC ichthyosis. The invention is useful in gene therapy and as vaccine. The
 CC present sequence is cytochrome P450 putative family signature peptide.
 CC This peptide is used in the exemplification of the invention

SQ Sequence 10 AA;

Query Match 100.0%; Score 33; DB 6; Length 10;

Best Local Similarity 40.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXCXG 10

Db 1 FXGXXXXCXG 10

Db 1 FGGGARSCLG 10

RESULT 13

AAE35262

ID AAE35262 standard; peptide; 10 AA.

XX AC AAE35262;

XX DT 28-MAY-2003 (first entry)

XX DE Cytochrome P450 putative family signature peptide #1.

XX DE Human; retinoic acid; vitamin A; cytochrome P450; actinic keratosis;

XX KW P450RA1; cancer; psoriasis; acne; ichthyosis; gene therapy; vaccine;

XX KW enzyme.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Misc-difference 2..3 /label= Unknown

XX FT Misc-difference 5..7 /label= Unknown

XX FT Misc-difference 9 /label= Unknown

XX FT WO200295034-A2.

XX PN 28-NOV-2002.

XX PD 23-MAY-2002; 2002WO-CA000758.

XX PF 23-MAY-2001; 2001US-0292531P.

XX PR (CYTO-) CYTOCHROMA INC.

XX PA Wisniewski J, Petkovich PM, Ramshaw H;

XX PI WPI; 2003-112152/10.

XX DR New isolated P450RA1-3 nucleic acid molecule and polypeptide, useful for

XX PT diagnosing, preventing, or treating disorders with aberrant expression or

XX PT activity of the P450RA1-3, such as cancer, actinic keratosis, acne and

XX PT psoriasis.

XX PS Example 1; Page 72; 23lpp; English.

XX CC The invention relates to retinoic acid metabolising cytochrome P450,

XX CC P450RA1 polypeptides and polynucleotides. Methods and compositions of the

XX CC invention are useful for diagnosing, preventing, ameliorating and/or

XX CC treating disorders associated with the aberrant expression or activity of

XX CC the P450RA1 such as diseases related to vitamin A and retinoic acid

XX CC metabolism, e.g. cancer, actinic keratosis, psoriasis, acne and

XX CC ichthyosis. The invention is useful in gene therapy and as vaccine. The

XX CC present sequence is cytochrome P450 putative family signature peptide.

XX CC This peptide is used in the exemplification of the invention

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 33; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10

Db 1 FXGXGXXCXG 10

RESULT 14

ADC56716

ID ADC56716 standard; peptide; 10 AA.

XX AC ADC56716;

XX DT 18-DEC-2003 (first entry)

XX DE Peptide 1 related to human vitamin-D3 hydroxylase.

XX KW vitamin-D3 hydroxylase; VDDH; antipsoriatic; osteopathic; hypercalcaemia;

XX KW gene therapy; antisense; hypoparathyroidism; rickets; psoriasis;

XX KW osteoporosis; renal insufficiency.

XX OS Unidentified.

XX PN JP2003047479-A.

XX PD 18-FEB-2003.

XX PF 08-AUG-2001; 2001JP-00241396.

XX PR 08-AUG-2001; 2001JP-00241396.

XX PA (MOCH) MOCHIDA PHARM CO LTD.

XX PA (HERI-) HERIKKUSU KENYUSHO KK.

XX DR WPI; 2003-508705/48.

XX PT Novel vitamin-D3 hydroxylase protein, useful for identifying modulators

XX PT of the vitamin-D3 hydroxylation activity of the enzyme.

XX PS Example 1; Page 10; 18pp; Japanese.

XX CC The invention relates to a novel vitamin-D3 hydroxylase (VDDH) protein.

XX CC The polypeptide of the invention demonstrates antipsoriatic and

XX CC osteopathic activities and may be useful for identifying compounds which

XX CC modulate the activity or inhibit the expression of vitamin-D3 hydroxylase

XX CC and thus for treating or preventing hypercalcaemia. Furthermore, the

XX CC polypeptide may be utilised during gene and antisense therapy, as well as

XX CC for treating activated vitamin-D3 deficiency disorders such as

XX CC hypoparathyroidism, rickets, psoriasis, osteoporosis and renal

XX CC insufficiency. The current sequence is that of the peptide 1 of the

XX CC invention which is related to human vitamin-D3 hydroxylase.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 33; DB 7; Length 10;

Best Local Similarity 40.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10

Db 1 FGHGVRSCIG 10

RESULT 15

ADC98703

ID ADC98703 standard; peptide; 10 AA.

XX AC ADC98703;

XX DT 01-JAN-2004 (first entry)

XX DE Cytochrome P450 haem ligand signature motif peptide.

XX KW ecdysteroid synthesis inhibitor; insecticidal; cytochrome P450;

XX KW haem ligand motif.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Misc-difference 2..3 /label= OTHER

XX FT Misc-difference 5..7 /note= "OTHER = Any amino acid"

XX FT Misc-difference 5..7 /label= OTHER

PT New expression vector comprising a nucleic acid sequence encoding a
PT polypeptide having monooxygenase P450 activity, useful in altering the
PT carotenoid production in a plant for enhancing production of specific
PT carotenoid compounds.
XX
PS Claim 7; SEQ ID NO 14; 135pp; English.
XX
CC The present invention relates to genes, proteins and methods comprising
CC carotenoid monooxygenases in the cytochrome P450 family. The invention
CC also relates to altering carotenoid ratios in plants and microorganisms
CC using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The
CC invention is useful in altering the carotenoid production in a plant for
CC enhancing production of specific carotenoid compounds that are potent
CC antioxidants. The present sequence is a cytochrome P450 monooxygenase
CC cysteine consensus motif peptide.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 33; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXXGXXXCXG 10
Db 1 FXXGXXXCXG 10
RESULT 18
ID AAR30867 standard; protein; 11 AA.
AC AAR30867;
XX
XX 25-MAR-2003 (revised)
DT 12-MAY-1993 (first entry)
XX
XX Consensus haem-binding domain of cyt-P450 in plants.
XX
XX Dihydrokaempferol; flavonoid; pigmentation; colour; amplification;
KW cytochrome P450; avocado; petunia; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 4 /label= Ala, Ser
FT Misc-difference 6 /label= Lys, Arg
FT Misc-difference 8 /label= Ile, Gly
XX
XX EP522880-A2.
PN
XX
PD 13-JAN-1993.
XX
XX 10-JUL-1992; 92EP-00306379.
XX
XX 11-JUL-1991; 91AU-00007173.
PR 17-FEB-1992; 92AU-00000923.
XX
XX (ITFL-) INT FLOWER DEV PTY LTD.
PA
XX Holton TA, Cornish EC, Kovacic F, Tanaka Y, Lester DR;
PI WPI; 1993-010688/02.
XX
XX Nucleic acid sequence encoding a di-hydro:kaempferol-hydroxylating enzyme
PT e.g. cytochrome P450 introduced into transgenic plants for controlling
PT flavonoid pigmentation in plants and organisms.
XX
PS Disclosure; Page 13; 66pp; English.
XX
XX The consensus sequence of haem-binding domains for avocado and petunia

CC cytochrome P450 homologues pCGP142 and pCGP147 was used to design
CC synthetic PCR primers. The primers may be used in PCR for amplification
CC of petal cytochrome P450 homologues. See also AAR30868-75. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 33; DB 2; Length 11;
Best Local Similarity 70.0%; Pred. No. 3.9e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXXGXXXCXG 10
Db 2 FGXGXRXCPG 11
RESULT 19
ID AAR40877 standard; protein; 11 AA.
XX
AC AAR40877;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX
XX SSP for flavonoid-3',5'-hydroxylase gene product.
XX
XX Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression; ss.
XX
XX Petunia x hybrida.
XX
XX WO9318155-A1.
PN
XX 16-SEP-1993.
PD
XX 20-NOV-1992; 92WO-JP001520.
PP
XX 02-MAR-1992; 92JP-00044963.
PR
XX (KYOW) KYOWA HAKKO KOGYO CO LTD.
PA
XX Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX
XX WPI; 1993-303469/38.
DR
XX N-PSDB; AAQ47878.
XX
XX Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
FT colour and altered pigment pattern.
XX
XX Claim 11; Page 58; 82pp; Japanese.
XX
XX Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 33; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXXGXXXCXG 10

PD 16-SEP-1993.
 XX 20-NOV-1992; 92WO-JP001520.
 XX 02-MAR-1992; 92JP-00044963.
 XX (KYOW) KYOWA HAKKO KOGYO CO LTD.
 XX Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
 XX Okinaka Y;
 XX WPI; 1993-303469/38.
 XX N-PSDB; AAQ47883.
 XX Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
 PT transform plants e.g. petunia, rose or tobacco to give bluer flower
 PT colour and altered pigment pattern.
 XX Claim 11; Page 60; 82pp; Japanese.
 XX Insertion of the sequences (AAQ47840-42) into plants such as rose,
 CC petunia, tobacco and carnation, using a suitable vector such as
 CC agrobacterium, give transformed plants which express the gene, resulting
 CC in petals with a bluer colour than normal, and/or pigmentation patterns
 CC which do not occur naturally. The sequences were amplified using primers
 CC (AAQ47843-70). Related single specific primers using a gene sequence
 CC coding for the haem-binding region of cytochrome P450 are shown in
 CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 24-OCT-2003 to standardise OS field)
 XX Query Match 100.0%; Score 33; DB 2; Length 11;
 XX Best Local Similarity 40.0%; Pred. No. 3.9e+02;
 XX Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FXXGXXXCXG 10
 |:::|::|
 Db 2 FSGGFCSCPG 11
 |:::|::|
 RESULT 23
 AAR40872
 ID AAR40872 standard; protein; 11 AA.
 XX AC AAR40872;
 XX 24-OCT-2003 (revised)
 XX 25-MAR-2003 (revised)
 XX 28-MAR-1994 (first entry)
 XX SSP for flavonoid-3',5'-hydroxylase gene product.
 XX Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
 XX tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
 XX polymerase chain reaction; amplification; expression.
 XX Petunia x hybrida.
 XX WO9318155-A1.
 XX 16-SEP-1993.
 XX 20-NOV-1992; 92WO-JP001520.
 XX 02-MAR-1992; 92JP-00044963.
 XX (KYOW) KYOWA HAKKO KOGYO CO LTD.
 XX Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
 XX Okinaka Y;
 XX WPI; 1993-303469/38.
 XX Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
 PT transform plants e.g. petunia, rose or tobacco to give bluer flower
 PT colour and altered pigment pattern.
 XX Claim 11; Page 60; 82pp; Japanese.
 XX Insertion of the sequences (AAQ47840-42) into plants such as rose,
 CC petunia, tobacco and carnation, using a suitable vector such as
 CC agrobacterium, give transformed plants which express the gene, resulting
 CC in petals with a bluer colour than normal, and/or pigmentation patterns
 CC which do not occur naturally. The sequences were amplified using primers
 CC (AAQ47843-70). Related single specific primers using a gene sequence
 CC coding for the haem-binding region of cytochrome P450 are shown in
 CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 24-OCT-2003 to standardise OS field)
 XX Query Match 100.0%; Score 33; DB 2; Length 11;
 XX Best Local Similarity 40.0%; Pred. No. 3.9e+02;
 XX Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FXXGXXXCXG 10
 |:::|::|
 Db 2 FSGGFCSCPG 11
 |:::|::|

DR N-PSDB; AAQ47873.
 XX Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
 PT transform plants e.g. petunia, rose or tobacco to give bluer flower
 PT colour and altered pigment pattern.
 XX Claim 11; Page 56; 82pp; Japanese.
 XX Insertion of the sequences (AAQ47840-42) into plants such as rose,
 CC petunia, tobacco and carnation, using a suitable vector such as
 CC agrobacterium, give transformed plants which express the gene, resulting
 CC in petals with a bluer colour than normal, and/or pigmentation patterns
 CC which do not occur naturally. The sequences were amplified using primers
 CC (AAQ47843-70). Related single specific primers using a gene sequence
 CC coding for the haem-binding region of cytochrome P450 are shown in
 CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 24-OCT-2003 to standardise OS field)
 XX Query Match 100.0%; Score 33; DB 2; Length 11;
 XX Best Local Similarity 40.0%; Pred. No. 3.9e+02;
 XX Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FXXGXXXCXG 10
 |:::|::|
 Db 2 FGAARRICPG 11
 |:::|::|
 RESULT 24
 AAR40879
 ID AAR40879 standard; protein; 11 AA.
 XX AC AAR40879;
 XX 24-OCT-2003 (revised)
 XX 25-MAR-2003 (revised)
 XX 28-MAR-1994 (first entry)
 XX SSP for flavonoid-3',5'-hydroxylase gene product.
 XX Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
 XX tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
 XX polymerase chain reaction; amplification; expression.
 XX Petunia x hybrida.
 XX WO9318155-A1.
 XX 16-SEP-1993.
 XX 20-NOV-1992; 92WO-JP001520.
 XX 02-MAR-1992; 92JP-00044963.
 XX (KYOW) KYOWA HAKKO KOGYO CO LTD.
 XX Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
 XX Okinaka Y;
 XX WPI; 1993-303469/38.
 XX N-PSDB; AAQ47880.
 XX Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
 PT transform plants e.g. petunia, rose or tobacco to give bluer flower
 PT colour and altered pigment pattern.
 XX Claim 11; Page 59; 82pp; Japanese.
 XX Insertion of the sequences (AAQ47840-42) into plants such as rose,
 CC petunia, tobacco and carnation, using a suitable vector such as
 CC agrobacterium, give transformed plants which express the gene, resulting
 CC in petals with a bluer colour than normal, and/or pigmentation patterns

CC which do not occur naturally. The sequences were amplified using primers
 CC (AAQ47843-70). Related single specific primers using a gene sequence
 CC coding for the haem-binding region of cytochrome P450 are shown in
 CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 24-OCT-2003 to standardise OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 33; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
 |::|::|::|
 Db 2 FGVGPRMCPG 11

RESULT 25
 AAR41632
 ID AAR41632 standard; protein; 11 AA.

XX AC AAR41632;

XX 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-MAR-1994 (first entry)

XX SSP for flavonoid-3',5'-hydroxylase gene product.

XX Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
 KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
 KW polymerase chain reaction; amplification; expression.

XX Petunia x hybrida.

XX WO9318155-A1.

XX 16-SEP-1993.

XX 20-NOV-1992; 92WO-JP001520.

XX 02-MAR-1992; 92JP-00044963.

XX (KYOW) KYOWA HAKKO KOGYO CO LTD.

XX Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;

XX Okinaka Y;

XX WPI; 1993-303469/38.

XX N-PSDB; AAQ47882.

XX Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
 PT transform plants e.g. petunia, rose or tobacco to give bluer flower
 PT colour and altered pigment pattern.

XX Claim 11; Page 60; 82pp; Japanese.

XX Insertion of the sequences (AAQ47840-42) into plants such as rose,
 CC petunia, tobacco and carnation, using a suitable vector such as
 CC agrobacterium, give transformed plants which express the gene, resulting
 CC in petals with a bluer colour than normal, and/or pigmentation patterns
 CC which do not occur naturally. The sequences were amplified using primers
 CC (AAQ47843-70). Related single specific primers using a gene sequence
 CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 24-OCT-2003 to standardise OS field.)
 XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 33; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
 |::|::|::|
 Db 2 FGVGPRMCPG 11

RESULT 26

AAR41634
 ID AAR41634 standard; protein; 11 AA.

XX AC AAR41634;

XX 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-MAR-1994 (first entry)

XX SSP for flavonoid-3',5'-hydroxylase gene product.

XX Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
 KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
 KW polymerase chain reaction; amplification; expression.

XX Petunia x hybrida.

XX WO9318155-A1.

XX 16-SEP-1993.

XX 20-NOV-1992; 92WO-JP001520.

XX 02-MAR-1992; 92JP-00044963.

XX (KYOW) KYOWA HAKKO KOGYO CO LTD.

XX Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;

XX Okinaka Y;

XX WPI; 1993-303469/38.

XX N-PSDB; AAQ47883.

XX Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
 PT transform plants e.g. petunia, rose or tobacco to give bluer flower
 PT colour and altered pigment pattern.

XX Claim 11; Page 61; 82pp; Japanese.

XX Insertion of the sequences (AAQ47840-42) into plants such as rose,
 CC petunia, tobacco and carnation, using a suitable vector such as
 CC agrobacterium, give transformed plants which express the gene, resulting
 CC in petals with a bluer colour than normal, and/or pigmentation patterns
 CC which do not occur naturally. The sequences were amplified using primers
 CC (AAQ47843-70). Related single specific primers using a gene sequence
 CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 24-OCT-2003 to standardise OS field.)
 XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 33; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
 |::|::|::|
 Db 2 FGVGPRMCPG 11

RESULT 27

AAR40873
 ID AAR40873 standard; protein; 11 AA.

XX AC AAR40873;

XX 24-OCT-2003 (revised)

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 2 FGAGRRICPG 11

RESULT 32

AAAR41635
ID AAR41635 standard; protein; 11 AA.

XX AC AAR41635;
XX XX

DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)

XX SSP for flavonoid-3',5'-hydroxylase gene product.

XX Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression.

XX Petunia x hybrida.

XX WO9318155-A1.

XX 16-SEP-1993.

XX 20-NOV-1992; 92WO-JP001520.

XX 02-MAR-1992; 92JP-00044963.

XX (KYOW) KYOWA HAKKO KOGYO CO LTD.

XX Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;

DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47885.

XX Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.

XX Claim 11; Page 61; 82pp; Japanese.

XX Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)

XX Sequence 11 AA;

Query Match 100.0%; Score 33; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 2 FGAGRRICPG 11

RESULT 33

AAAR40875
ID AAR40875 standard; protein; 11 AA.

XX AC AAR40875;
XX XX

DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX SSP for flavonoid-3',5'-hydroxylase gene.
XX Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression; ss.
XX Petunia x hybrida.
XX WO9318155-A1.
XX 16-SEP-1993.
XX 20-NOV-1992; 92WO-JP001520.
XX 02-MAR-1992; 92JP-00044963.
XX (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX WPI; 1993-303469/38.
XX N-PSDB; AAQ47876.
XX Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX Claim 11; Page 57; 82pp; Japanese.
XX Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)

Query Match 100.0%; Score 33; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 2 FGAGRRICPG 11

RESULT 34
AAU80018
ID AAU80018 standard; peptide; 11 AA.
XX AC AAU80018;
XX 15-JUL-2002 (first entry)
XX Conserved haem-binding domain of P450 proteins.
DE Plant; aspen; phenylpropanoid pathway; agronomic; lignin; paper;
XX 4-coumarate-CoA ligase; 4CL; coniferyl aldehyde 5-hydroxylase; CAlid5H;
KW S-adenosyl-L-methionine-dependent; SAM; AldOMT; transgenic; grass;
KW 5-hydroxyconiferaldehyde O-methyltransferase; cellulose; pulp;
KW coniferyl alcohol dehydrogenase; CAD; sinapyl alcohol dehydrogenase; SAD;
KW syringyl; guaiacyl; agriculture; haem-binding domain; P450.
XX Synthetic.
OS

XX Key Location/Qualifiers
 FT Misc-difference 4 /label= unknown
 FT Misc-difference 6 /label= unknown
 FT Misc-difference 7 /label= unknown
 FT Misc-difference 8 /label= unknown
 FT Misc-difference 10 /label= unknown
 FT FT
 XX WO200220717-A2.
 XX 14-MAR-2002.
 XX 05-SEP-2001; 2001WO-US027445.
 XX 05-SEP-2000; 2000US-0230086P.
 XX (UNMT) UNIV MICHIGAN TECHNOLOGICAL.
 XX PA Chiang VLC, Li L;
 XX PI WPI; 2002-351773/38.

Genetically transforming plant with multiple genes from phenylpropanoid pathways, comprises incorporating number of genes into the genome of the plant, to produce plants displaying altered agronomic traits.

Disclosure; Page 6; 95pp; English.

The invention relates to a method of genetically transforming a plant simultaneously with multiple genes from the phenylpropanoid pathways, comprising incorporating into the genome of the plant, a number of genes, their substantially similar fragments or their combinations, to produce plants displaying altered agronomic traits. The genes are selected from 4 -coumarate-CoA ligase (4CL), coniferyl aldehyde 5-hydroxylase (CAlD5H), s-adenosyl-L-methionine (SAM)-dependent 5-hydroxyconifer aldehyde O-methyltransferase (AldOMT), coniferyl alcohol dehydrogenase (CAD) and sinapyl alcohol dehydrogenase (SAD). The method is useful for the transformation of plant tissue for the alteration of lignin monomer composition, increased syringyl/guaiacyl (S/G) lignin ratio and increased cellulose content and transgenic plants resulting from such transformations. This is an improved method to simultaneously control the lignin quantity, lignin compositions, and cellulose contents in plants, and is applicable to all plant species that are susceptible to the transfer of genetic information by Agrobacterium or other gene delivery system. The method is of particular value to paper and pulp industries because lignin containing higher syringyl monomer content is more susceptible to chemical delignification. Woody plants transformed with DNA constructs offer a significant advantage in the delignification process over conventional paper feedstocks. Similarly, modification of the lignin composition in grasses by insertion and expression of heterologous SAD gene offers a unique method for increasing the digestibility of grasses and is of significant potential economic benefit to the farm and agricultural industries. The present sequence represents the amino acid sequence of the conserved haem-binding domain of P450 proteins, which has homology to CAlD5H as described in the method of the invention

Sequence 11 AA;

Query Match 100.0%; Score 33; DB 5; Length 11;
 Best Local Similarity 90.0%; Pred. No. 3.9e+02;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
 |:|||||
 Db 2 FGXGXXXCXG 11

RESULT 35
 ADO58606
 ID ADO58606 standard; peptide; 11 AA.
 XX AC ADO58606;
 XX DT 15-JUL-2004 (first entry)
 XX DE Pepper cytochrome P450 (pepCYP) associated peptide.
 XX KW Pepper; cytochrome P450; pepCYP; incompatible interaction.
 XX OS Unidentified.
 XX Key Location/Qualifiers
 FT Misc-difference 1.11
 FT /note= "All Xaa residues are unknown"
 XX KR2001081198-A.
 XX 29-AUG-2001.
 XX 11-FEB-2000; 2000KR-00006345.
 XX 11-FEB-2000; 2000KR-00006345.
 XX (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
 XX PI Kim YS, Ko MG, Oh BJ;
 XX WPI; 2002-128887/17.
 XX Pepper cytochrom p450 gene(pepCYP) highly expressed during incompatible interaction between colletotrichum gloeosporioides and peppers.
 XX Disclosure; Page 2; 16pp; Korean.
 CC The present invention relates to the isolation of a pepper (Capsicum annuum) cytochrome P450 gene (PepCYP), which is highly expressed by incompatible interaction between Colletotrichum gloeosporioides and peppers. The present peptide sequence of unknown function is given in the specification of the present invention.
 XX SQ Sequence 11 AA;
 Query Match 100.0%; Score 33; DB 5; Length 11;
 Best Local Similarity 80.0%; Pred. No. 3.9e+02;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FXXGXXXCXG 10
 |:|||||
 Db 2 FGXGXXXCXG 11
 RESULT 36
 AAE30014
 ID AAE30014 standard; peptide; 11 AA.
 XX AC AAE30014;
 XX DT 24-FEB-2003 (first entry)
 XX Cytochrome P450 protein conserved domain #3.
 KW Tobacco; plant; cytochrome P450; disease resistance; biosynthesis; lipid; hormone; insect attractant; secondary metabolite; herbicide; pesticide;
 KW pollutant; deterrent; insect predator; flavouring; antibacterial;
 KW fungicide; viricide; insecticide.
 XX OS Nicotiana tabacum.
 XX Key Location/Qualifiers
 FT Misc-difference 4

CC Solanaceae crop plants. Transgenic plants comprising DNA constructs
 CC having the P450 encoding nucleic acid sequences are resistant to
 CC phenylurea herbicides. The transgenic plants have increased resistance to
 CC phenylurea herbicides compared to wild-type plants of the same species.
 CC The plant crops, e.g. turfgrass, tobacco, potato, corn, rice,
 CC cotton, soybean, rape, wheat, oats, barley or rice are particularly
 CC resistant to flumeturon, linuron, chlortoluron or diuron

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 33; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 4.5e+02;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXXCG 10
 |:|:|:|:|
 Db 4 FGXGXXCG 13

RESULT 39

AAB11394
 ID AAB11394 standard; protein; 13 AA.

XX AC AAB11394;

DT 12-SEP-2003 (revised)
 DT 22-FEB-2001 (first entry)

XX Gerbera flavone synthase FNSII haem-binding peptide fragment.

XX Gerbera; transgenic plant; flavone synthase II; FNSII; anticancer;
 KW immunomodulator; naringenin; apigenin; ornamental plant; flower colour;
 KW pharmaceutical; cancer; treatment.

XX Gerbera hybrid cultivar.

XX DE19918365-A1.

XX 26-OCT-2000.

XX 22-APR-1999; 99DE-01018365.

XX 22-APR-1999; 99DE-01018365.

XX (MART/) MARTENS S.

XX (FORK/) FORKMANN G.

XX Martens S, Forkmann G;

XX WPI; 2000-648348/63.

XX New nucleic acid encoding flavone synthase II, useful e.g. for producing
 XX transgenic plants with altered flower color or flavone content.

XX Disclosure; Fig 4A; 40pp; German.

XX This invention describes a novel nucleic acid (I) that encodes flavone
 CC synthase II (FNSII) which has anticancer and immunomodulatory activity.
 CC FNSII catalyzes conversion of naringenin to apigenin. (I) is used to
 CC produce transgenic ornamental plants that have targeted alterations in
 CC flower color, also altered content/distribution of flavones in leaves,
 CC flowers and other tissues, e.g. increased resistance properties or
 CC symbiotic capacity. FNSII expressed by (I) is used in synthesis of
 CC flavones that are useful as pharmaceuticals, e.g. in cancer treatment, or
 CC as biologically active substances, e.g. to improve the immune defence
 CC system. Oligonucleotide fragments of (I) are used as probes and primers,
 CC or as antisense or ribozyme agents for regulating expression of (II).
 CC (Updated on 12-SEP-2003 to standardise OS field)

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 33; DB 3; Length 13;

Best Local Similarity 70.0%; Pred. No. 4.5e+02;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FXGXXXXXCG 10
 |:|:|:|:|
 Db 3 FGXGXXCG 12

RESULT 40

AAG98132
 ID AAG98132 standard; peptide; 14 AA.

XX AC AAG98132;

DT 19-SEP-2001 (first entry)

DE Human SNP associated peptide SEQ ID NO. 774.

XX Human; single nucleotide polymorphism; SNP; angiotensin;
 KW 4-hydroxybutyrate; dehydrogenase; protein therapy;
 KW adenosine triphosphate-dependent RNA helicase;

XX major histocompatibility complex Class I histocompatibility antigen; MHC;
 KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;
 KW antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
 KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.

XX Homo sapiens.

XX WO200148245-A2.

XX 05-JUL-2001.

XX 27-DEC-2000; 2000WO-US035346.

XX 27-DEC-1999; 99US-00472688.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-418297/44.

XX Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
 PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
 PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
 PT diseases and infections.

XX Disclosure; Page 461; 484pp; English.

XX The invention relates to nucleic acids (AAH79386-AAH80036) encoding
 CC polymorphic variants of proteins (AAG98010-AAG98238) related to
 CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
 CC ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
 CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
 CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
 CC proteins have potential immunosuppressive, immunostimulatory,
 CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
 CC antileukemic, neuroprotective and antimicrobial activity and may be
 CC useful in gene/protein therapy, vaccines, modulation of the expression
 CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,
 CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major
 CC histocompatibility complex (MHC) Class I histocompatibility antigen
 CC and/or phosphoglycerate kinase. Disorders that may be prevented,
 CC diagnosed and/or treated by the above methods include multifactorial
 CC diseases with a genetic component, such as autoimmune diseases (e.g.
 CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
 CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of
 CC the bladder, brain, breast, colon and kidney, leukemia), diseases of the
 CC nervous system, an infection of pathogenic organisms. They may also be
 CC used to alter phenotypic traits such as longevity, appearance, strength,
 CC speed and endurance

XX SQ Sequence 14 AA;

Best Local Similarity 40.0%; Pred. No. 5.1e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|:|:|:|:|:
Db 4 FLGGTTVCLG 13

RESULT 46

AAAB19305
ID AAB19305 standard; peptide; 15 AA.

XX AC AAB19305;

XX DT 19-FEB-2001 (first entry)

XX DE Immunogenic peptide useful for generating antigen specific T cells.

XX KW Immunogenic peptide; antigen specific T cell; cell proliferation; cancer;
KW inflammation; autoimmune disease; dermatological disorder;
KW neurodegenerative disorder; atherosclerosis; rheumatoid arthritis;
KW osteoporosis; chronic ulcer; psoriasis; cardiovascular disease;
KW infectious disease.

XX OS Hepatitis A virus.

XX FN WO200057920-A2.

XX PD 05-OCT-2000.

XX PF 30-MAR-2000; 2000WO-GB001225.

XX PR 30-MAR-1999; 99GB-00007366.

XX PA (MEDI-) MEDICAL RES COUNCIL.

XX PI Fisher A;

XX WPI; 2000-647208/62.

XX DR Regulating expression of transgenes encoding enzymes or hormones in
XX PT mammals, by transforming expandable population of cells with desired
XX PT transgene and regulating cell proliferation by administration of an
XX PT agent.

XX PS Disclosure; Page 22; 37pp; English.

XX CC The present sequence represents an immunogenic peptide, derived from the
XX CC S antigen, which is useful for generating antigen specific T cells. It
XX CC may be used in the course of the invention. The specification describes
XX CC the use of an agent which regulates cell proliferation for modulating the
XX CC levels of production of a gene product of interest in a host organism.
XX CC The method comprises transforming an expandable population of cells with
XX CC a transgene encoding the gene product, expressing the gene in the host
XX CC and regulating proliferation of the population of cells by administration
XX CC of the agent. The method is useful for regulating cell proliferation. The
XX CC method is also useful for delivering one or more transgenes useful in the
XX CC treatment of cancer, inflammation, autoimmune disease, dermatological
XX CC disorder, neurodegenerative disorder, atherosclerosis, rheumatoid
XX CC arthritis, osteoporosis, chronic ulcers, psoriasis, cardiovascular
XX CC diseases and infectious diseases

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 33; DB 3; Length 15;

Best Local Similarity 40.0%; Pred. No. 5.1e+02;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|:|:|:|:|:
Db 4 FLGGTTVCLG 13

RESULT 47

AAU91319
ID AAU91319 standard; peptide; 15 AA.

XX AC AAU91319;

XX DT 18-JUN-2002 (first entry)

XX DE Cytochrome P450 haeme binding motif.

XX KW Thymus expressed cytochrome; arachidonic acid metabolism;

XX KW autoimmune disorder; Addison's disease; haemolytic anaemia;

XX KW rheumatoid arthritis; dermatitis; allergic encephalomyelitis;

XX KW glomerulonephritis; Goodpasture's Syndrome; Grave's disease;

XX KW multiple sclerosis; myasthenia gravis; neuritis; organ rejection;

XX KW systemic lupus erythematosus; insulin dependent diabetes mellitus;

XX KW autoimmune inflammatory eye disease; graft versus-host disease;

XX KW inflammatory disease; infection; septic shock; sepsis; SIRS;

XX KW systemic inflammatory response syndrome; ischaemia reperfusion injury;

XX KW arthritis; inflammatory bowel disease; Crohn's disease; thymoma; P450TEC;

XX KW immune system disease; haeme binding motif.

XX OS Unidentified.

XX PN WO200181585-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-CA000547.

XX PR 20-APR-2000; 2000US-0198617P.

XX PR 01-JUN-2000; 2000US-0208785P.

XX PA (CYTO-) CYTOCHROME INC.

XX PI Jones G, Petkovich PM, White JA, Ramshaw HA, Stangle WA;

XX WPI; 2002-291654/33.

XX PT New human cytochrome P450TEC, thymus expressed cytochrome polypeptides
XX PT for diagnosing, treating autoimmune disorders e.g. Addison's disease,
XX PT dermatitis, rheumatoid arthritis and identifying modulators.

XX PS Example 1; Page 65; 154pp; English.

XX CC The invention relates to an isolated human cytochrome P450TEC (thymus
XX CC expressed cytochrome) polypeptide or the encoded sequence included in
XX CC ATCC Deposit No. PTA-1785. Also included are the polynucleotide encoding
XX CC P450TEC, its allelic variants, complement, or species homologue, where
XX CC the nucleic acid can modulate, or encodes a peptide that modulates
XX CC arachidonic acid metabolism and hydroxylation of arachidonic acid.
XX CC P450TEC is useful for treating disease or condition related to P450TEC
XX CC and for identifying an activity in a biological assay, by expressing
XX CC P450TEC in a cell, isolating the biological fraction, detecting an
XX CC activity in a biological assay and identifying the protein in the
XX CC supernatant having the activity. The nucleic acid is useful for diagnosis
XX CC of P450TEC-related disease or condition, in particular autoimmune
XX CC disease, a disease related to hydroxylation pathway of arachidonic acid
XX CC or inflammatory response of a patient or a predisposition to the disease
XX CC by detecting a polymorphism in P450TEC gene. P450TEC is useful for
XX CC identifying modulators of P450TEC activity. An anti-P450TEC antibody is
XX CC useful for quantifying the level of P450TEC in a sample and for treating
XX CC disease or condition related to P450TEC. P450TEC polynucleotides or
XX CC polypeptides are useful as marker or detector of a particular immune
XX CC system disease or disorder and in treating or detecting autoimmune
XX CC disorders including Addison's disease, haemolytic anaemia, rheumatoid
XX CC arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis,
XX CC Goodpasture's Syndrome, Grave's disease, multiple sclerosis, myasthenia
XX CC gravis, neuritis, systemic lupus erythematosus, insulin dependent
XX CC diabetes mellitus, autoimmune inflammatory eye disease and organ
XX CC rejection or graft versus-host disease. P450TEC is useful for diagnosis
XX CC or analysis of disease states involving P450TEC or to monitor progress of
XX CC therapy. P450TEC antagonists are useful to treat disorders such as acute

CC and chronic inflammatory diseases, including inflammation associated with
 CC infection (e.g. septic shock, sepsis, systemic inflammatory response
 CC syndrome (SIRS)), ischemia reperfusion injury, arthritis, inflammatory
 CC bowel disease, Crohn's disease and conditions of the thymus, such as
 CC thymomas. The present sequence is a cytochrome haeme binding motif used
 CC in sequence similarity searches to identify nucleic acid sequences
 CC encoding P450TEC

XX Sequence 15 AA;

Query Match 100.0%; Score 33; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
 |||||
 Db 2 FXXGXXXCXG 11

RESULT 48

ID ABG75617 standard; peptide; 15 AA.

XX AC ABG75617;

DT 16-APR-2003 (first entry)

XX Arabidopsis thaliana cytochrome P450 protein peptide fragment #5.

XX Arabidopsis; cytochrome P450; cp450; plant; parthenocarpic; fruit;
 KW enlarged fruit; transgenic; vegetable size; grain size; soybean;
 KW leaf size; flower size; agricultural yield; male-sterile plant;
 KW moth orchid; maize.

XX Arabidopsis thaliana.

OS Glycine max.

OS Pinus radiata.

OS Zea mays.

OS Phalaenopsis sp.

XX Key Location/Qualifiers

FT Misc-difference 7 /label= Ala, Ser

FT Misc-difference 9 /label= Arg, Lys

FT Misc-difference 11 /label= Val, Ile, Ala

FT /label= Val, Ile, Ala

XX US2002152495-A1.

XX 17-OCT-2002.

XX 09-JUL-1999; 99US-00349385.

XX 15-JAN-1999; 99US-0115967P.

XX (ITOT/) ITO T.

XX (FROM/) FROMM M.

XX (MEYE/) MEYEROWITZ E.

XX Ito T, Fromm M, Meyerowitz E;

XX WPI; 2003-198390/19.

XX New polynucleotides encoding a cytochrome P450 polypeptide, useful for
 PT producing plants with enlarged or parthenocarpic fruits, in increasing
 PT plant tissue size to increase agricultural yields, or producing male-
 PT sterile plants.

XX Disclosure; Page 3; 31pp; English.

XX This invention relates to an isolated polynucleotide encoding a
 CC cytochrome P450 polypeptide which when expressed in a plant produces at

CC least one phenotype selected from parthenocarpic fruit and enlarged
 CC fruit. The invention also discloses a recombinant construct comprising
 CC the novel polynucleotide which when expressed in a plant produces a plant
 CC with a parthenocarpic fruit or enlarged fruit. Also disclosed is a
 CC transgenic plant which expresses a cytochrome P450 or comprising an
 CC isolated polynucleotide encoding a cytochrome P450 polypeptide which when
 CC expressed in a plant produces a plant with a parthenocarpic fruit or
 CC enlarged fruit compared with a plant lacking the isolated polynucleotide.
 CC The cytochrome P450 polypeptide and polynucleotide of the invention is
 CC useful in the production of plants with seedless, enlarged, or
 CC parthenocarpic fruits, including vegetable or grain size, leaf size or
 CC flower size. The sequences may also be used in increasing plant tissue
 CC size to increase agricultural yields of plants, to produce male-sterile
 CC plants and to screen for compounds that control parthenocarp or fruit
 CC size in plants. The present sequence represents a cytochrome P450 peptide
 CC of the invention, this sequence is highly conserved in cytochrome P450
 CC proteins

XX Sequence 15 AA;

Query Match 100.0%; Score 33; DB 6; Length 15;
 Best Local Similarity 70.0%; Pred. No. 5.1e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10

||:|||||

Db 5 FGXGXRCXCPG 14

RESULT 49

ADV23624

ID ADV23624 standard; peptide; 15 AA.

XX AC ADV23624;

DT 10-MAR-2005 (first entry)

XX HBV immunogenic peptide #425.

KW Vaccine; virucide; antigen; autoimmune disease; infection;
 KW immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
 KW breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
 KW pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
 KW hodgkin's lymphoma.

XX Hepatitis B virus.

XX WO2004108753-A1.

XX 16-DEC-2004.

XX 10-JUN-2004; 2004WO-AU000775.

XX 10-JUN-2003; 2003AU-00902875.

XX 25-MAR-2004; 2004AU-00901589.

XX (UYME) UNIV MELBOURNE.

XX Kent SJ;

XX WPI; 2005-031657/03.

XX Use of at least one set of peptides in the preparation of a medicament
 PT for modulating an immune response, and for treating cancer or yeast,
 PT viral, bacterial, protozoal and mycoplasma infections.

XX Disclosure; SEQ ID NO 2044; 645pp; English.

XX The invention relates to the use of at least one set of peptides in the
 CC preparation of a medicament for modulating an immune response, where
 CC individual peptides of a respective set comprise different portions of an
 CC amino acid sequence corresponding to a single polypeptide of interest and
 CC display partial sequence identity or similarity to at least one other

peptide of the same set of peptides (i.e. they are overlapping). Also included are an antigen-presenting cell which has been contacted with the peptides above and thus presents the peptides, a population of such antigen-presenting cells, a process for producing antigen-presenting cells for modulating an immune response to a polypeptide of interest, a method for producing antigen-specific lymphocytes, a composition comprising at least one set of the peptides (and a carrier and/or diluent), a method for modulating an immune response to a polypeptide of interest comprising administering to a patient in need at least one set of the peptides, a method for treatment and/or prophylaxis of a disease or condition associated with the presence of a polypeptide of interest and a composition of matter for modulating an immune response in a disease- or condition-associated polypeptide that is a polypeptide produced by a pathogenic organism or a cancer, and produced by a pathogenic organism selected from yeast, viruses, bacteria, helminths, protozoans and mycoplasmas. The disease- or condition-associated polypeptide is produced by a cancer selected from melanoma, lung cancer, breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic cancer, stomach cancer, bladder cancer, kidney cancer, post transplant lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncultured antigen-presenting cells or their precursors are useful in the preparation of a medicament for the treatment of a disease or condition in a subject, which disease or condition is associated with the presence of the target antigen, where the antigen-presenting cells or their precursors have not been subjected to activating conditions but have been contacted with an antigen that corresponds to the target antigen to express a processed or modified form of the antigen for presentation to the subject's immune system. The present sequence is one of a set of overlapping immunogenic peptides derived from a Hepatitis B virus protein.

Sequence 15 AA;

Query Match 100.0%; Score 33; DB 9; Length 15;
Best Local Similarity 40.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 2 FLGGTTVCLG 11

RESULT 50
ADV23625
ID ADV23625 standard; peptide; 15 AA.

XX AC ADV23625;

XX DT 10-MAR-2005 (first entry)

XX DE HBV immunogenic peptide #426.

XX KW Vaccine; viricide; antigen; autoimmune disease; infection;
KW immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
KW breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
KW pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
KW hodgekin's lymphoma.

XX OS Hepatitis B virus.

XX FN WO2004108753-A1.

XX XX 16-DEC-2004.

XX XX 10-JUN-2004; 2004WO-AU000775.

XX XX 10-JUN-2003; 2003AU-00902875.

XX PR 25-MAR-2004; 2004AU-00901589.

XX PA (UYME) UNIV MELBOURNE.

XX PJ Kent SJ;

XX DR WPI; 2005-031657/03.

XX PT Use of at least one set of peptides in the preparation of a medicament
PT for modulating an immune response, and for treating cancer or yeast,
PT viral, bacterial, protozoal and mycoplasma infections.

XX PS Disclosure; SEQ ID NO 2045; 645pp; English.

XX CC The invention relates to the use of at least one set of peptides in the
CC preparation of a medicament for modulating an immune response, where
CC individual peptides of a respective set comprise different portions of an
CC amino acid sequence corresponding to a single polypeptide of interest and
CC display partial sequence identity or similarity to at least one other
CC peptide of the same set of peptides (i.e. they are overlapping). Also
CC included are an antigen-presenting cell which has been contacted with the
CC peptides above and thus presents the peptides, a population of such
CC antigen-presenting cells, a process for producing antigen-presenting
CC cells for modulating an immune response to a polypeptide of interest, a
CC method for producing antigen-specific lymphocytes, a composition
CC comprising at least one set of the peptides (and a carrier and/or
CC diluent), a method for modulating an immune response to a polypeptide of
CC interest comprising administering to a patient in need at least one set
CC of the peptides, a method for treatment and/or prophylaxis of a disease
CC or condition associated with the presence of a polypeptide of interest
CC and a composition of matter for modulating an immune response in a
CC subject to a target antigen. The polypeptide of interest is also a
CC disease- or condition-associated polypeptide that is a polypeptide
CC produced by a pathogenic organism or a cancer, and produced by a
CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
CC protozoans and mycoplasmas. The disease- or condition-associated
CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncultured
CC antigen-presenting cells or their precursors are useful in the
CC preparation of a medicament for the treatment of a disease or condition
CC in a subject, which disease or condition is associated with the presence
CC of the target antigen, where the antigen-presenting cells or their
CC precursors have not been subjected to activating conditions but have
CC been contacted with an antigen that corresponds to the target antigen
CC for presentation to the subject's immune system. The present sequence is
CC one of a set of overlapping immunogenic peptides derived from a Hepatitis
CC B virus protein.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 33; DB 9; Length 15;
Best Local Similarity 40.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 3 FLGGAPTCPG 12

Search completed: March 8, 2006, 11:19:58
Job time : 194 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 8, 2006, 11:25:42 ; Search time 23 Seconds
(without alignments)
12.102 Million cell updates/sec

Title: US-10-751-235-14

Perfect score: 33

Sequence: 1 FXXGXXXCXG 10

Scoring table: #BL0SUM62DXC

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.New.*

1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*

2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*

5: /cgn2_6/ptodata/2/pubppaa/US05_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*

7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	10	7	US-11-166-609-24
2	33	100.0	10	7	US-11-166-609-25
3	33	100.0	52	7	US-11-205-109-43
4	33	100.0	61	7	US-11-096-568A-25378
5	33	100.0	71	7	US-11-087-099-10778
6	33	100.0	73	7	US-11-116-881A-542
7	33	100.0	73	7	US-11-116-881A-546
8	33	100.0	75	6	US-10-467-657-8472
9	33	100.0	84	6	US-10-453-372-494
10	33	100.0	86	7	US-11-116-881A-548
11	33	100.0	99	7	US-11-096-568A-25377
12	33	100.0	101	7	US-11-116-881A-2299
13	33	100.0	103	7	US-11-072-512-3124
14	33	100.0	107	7	US-11-096-568A-26958
15	33	100.0	113	6	US-10-821-234-1478
16	33	100.0	117	7	US-11-087-099-6613
17	33	100.0	118	7	US-11-116-881A-464
18	33	100.0	119	7	US-11-116-881A-460
19	33	100.0	128	7	US-11-072-512-2610
20	33	100.0	128	7	US-11-166-609-14
21	33	100.0	128	7	US-11-166-609-15
22	33	100.0	129	7	US-11-116-881A-500
23	33	100.0	129	7	US-11-116-881A-516
24	33	100.0	129	7	US-11-116-881A-540
25	33	100.0	134	7	US-11-143-980-68

26	33	100.0	135	7	US-11-116-881A-456	Sequence 456, App
27	33	100.0	137	7	US-11-116-881A-520	Sequence 520, App
28	33	100.0	140	7	US-11-116-881A-462	Sequence 462, App
29	33	100.0	141	7	US-11-084-508-22	Sequence 22, Appl
30	33	100.0	151	7	US-11-116-881A-448	Sequence 448, App
31	33	100.0	151	7	US-11-116-881A-510	Sequence 510, App
32	33	100.0	155	7	US-11-096-568A-12468	Sequence 12468, A
33	33	100.0	156	7	US-11-096-568A-14864	Sequence 14864, A
34	33	100.0	158	7	US-11-096-568A-14863	Sequence 14863, A
35	33	100.0	162	7	US-11-116-881A-486	Sequence 486, App
36	33	100.0	164	7	US-11-116-881A-484	Sequence 484, App
37	33	100.0	175	7	US-11-116-881A-470	Sequence 470, App
38	33	100.0	176	7	US-11-120-308-106	Sequence 106, App
39	33	100.0	177	7	US-11-116-881A-522	Sequence 522, App
40	33	100.0	177	7	US-11-116-881A-502	Sequence 502, App
41	33	100.0	185	6	US-10-467-657-1228	Sequence 1228, Ap
42	33	100.0	187	7	US-11-116-881A-458	Sequence 458, App
43	33	100.0	194	7	US-11-096-568A-23881	Sequence 23881, A
44	33	100.0	197	7	US-11-096-568A-18243	Sequence 18243, A
45	33	100.0	199	5	US-09-995-493-12	Sequence 12, Appl
46	33	100.0	208	7	US-11-087-099-7405	Sequence 7405, Ap
47	33	100.0	208	7	US-11-087-099-11148	Sequence 11148, A
48	33	100.0	210	7	US-11-096-568A-23880	Sequence 23880, A
49	33	100.0	213	7	US-11-087-099-2635	Sequence 2635, Ap
50	33	100.0	213	7	US-11-087-099-11719	Sequence 11719, A
51	33	100.0	213	7	US-11-096-568A-20260	Sequence 20260, A
52	33	100.0	219	7	US-11-096-568A-24257	Sequence 24257, A
53	33	100.0	221	7	US-11-096-568A-27263	Sequence 27263, A
54	33	100.0	222	7	US-11-019-711-81	Sequence 81, Appl
55	33	100.0	222	7	US-11-087-099-6134	Sequence 6134, Ap
56	33	100.0	222	7	US-11-096-568A-28174	Sequence 28174, A
57	33	100.0	224	7	US-11-087-099-8664	Sequence 8664, Ap
58	33	100.0	225	7	US-11-096-568A-32197	Sequence 32197, A
59	33	100.0	226	7	US-11-148-012-2	Sequence 2, Appl
60	33	100.0	226	7	US-11-148-012-3	Sequence 3, Appl
61	33	100.0	229	7	US-11-096-568A-32196	Sequence 32196, A
62	33	100.0	233	7	US-11-096-568A-24646	Sequence 24646, A
63	33	100.0	234	7	US-11-096-568A-15121	Sequence 15121, A
64	33	100.0	237	7	US-11-096-568A-24645	Sequence 24645, A
65	33	100.0	237	7	US-11-096-568A-31128	Sequence 31128, A
66	33	100.0	240	7	US-11-019-711-76	Sequence 76, Appl
67	33	100.0	240	7	US-11-087-099-1831	Sequence 1831, Ap
68	33	100.0	241	7	US-11-019-711-22	Sequence 22, Appl
69	33	100.0	241	7	US-11-019-711-77	Sequence 77, Appl
70	33	100.0	241	7	US-11-019-711-78	Sequence 78, Appl
71	33	100.0	241	7	US-11-234-786-114	Sequence 114, App
72	33	100.0	242	7	US-11-096-568A-31127	Sequence 31127, A
73	33	100.0	247	7	US-11-019-711-79	Sequence 79, Appl
74	33	100.0	250	7	US-11-096-568A-18242	Sequence 18242, A
75	33	100.0	251	7	US-11-087-099-1436	Sequence 1436, Ap
76	33	100.0	252	7	US-11-096-568A-20380	Sequence 20380, A
77	33	100.0	253	7	US-11-096-568A-31126	Sequence 31126, A
78	33	100.0	256	7	US-11-116-881A-482	Sequence 482, App
79	33	100.0	260	7	US-11-096-568A-24256	Sequence 24256, A
80	33	100.0	270	6	US-10-453-372-462	Sequence 462, App
81	33	100.0	270	6	US-10-453-372-464	Sequence 464, App
82	33	100.0	271	7	US-11-096-568A-15685	Sequence 15685, A
83	33	100.0	272	7	US-11-037-243-99	Sequence 99, Appl
84	33	100.0	272	7	US-11-096-568A-18241	Sequence 18241, A
85	33	100.0	274	7	US-11-072-512-2191	Sequence 2191, Ap
86	33	100.0	274	7	US-11-096-568A-15773	Sequence 15773, A
87	33	100.0	274	7	US-11-096-568A-20855	Sequence 20855, A
88	33	100.0	275	7	US-11-087-099-6038	Sequence 6038, Ap
89	33	100.0	276	7	US-11-096-568A-15772	Sequence 15772, A
90	33	100.0	280	7	US-11-096-568A-15120	Sequence 15120, A
91	33	100.0	281	6	US-10-934-944-387	Sequence 387, App
92	33	100.0	281	6	US-10-980-556-12	Sequence 12, Appl
93	33	100.0	281	7	US-11-116-881A-2298	Sequence 2298, Ap
94	33	100.0	282	6	US-10-980-556-16	Sequence 16, Appl
95	33	100.0	282	7	US-11-096-568A-28790	Sequence 28790, A
96	33	100.0	286	7	US-11-087-099-5131	Sequence 5131, Ap
97	33	100.0	286	7	US-11-096-568A-15684	Sequence 15684, A
98	33	100.0	293	7	US-11-096-568A-23769	Sequence 23769, A

99 33 100.0 299 7 US-11-096-568A-20853 Sequence 20853, A
100 33 100.0 312 7 US-11-096-568A-34393 Sequence 34393, A

ALIGNMENTS

RESULT 1
US-11-166-609-24
; Sequence 24, Application US/11166609
; Publication No. US20060015968A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMNELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; TITLE OF INVENTION: METHOD OF USING SAME
; FILE REFERENCE: 1148CR
; CURRENT APPLICATION NUMBER: US/11/166,609
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 10/412,000
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 09/670,153
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)..(3)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Variable amino acid
US-11-166-609-24

Query Match 100.0%; Score 33; DB 7; Length 10;
Best Local Similarity 90.0%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|||||

Db 1 FXGXGXXCXG 10

RESULT 2
US-11-166-609-25
; Sequence 25, Application US/11166609
; Publication No. US20060015968A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMNELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; TITLE OF INVENTION: METHOD OF USING SAME
; FILE REFERENCE: 1148CR
; CURRENT APPLICATION NUMBER: US/11/166,609
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 10/412,000

; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 09/670,153
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Zea mays
US-11-166-609-25

Query Match 100.0%; Score 33; DB 7; Length 10;
Best Local Similarity 40.0%; Pred. No. 19;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|

Db 1 FQAGPRICLG 10

RESULT 3
US-11-205-109-43
; Sequence 43, Application US/11205109
; Publication No. US20050287641A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
; FILE REFERENCE: 3002-2US
; CURRENT APPLICATION NUMBER: US/11/205,109
; CURRENT FILING DATE: 2005-08-17
; PRIOR APPLICATION NUMBER: US/09/976,059
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,924
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 52
; TYPE: PRT
; ORGANISM: bacteria
US-11-205-109-43

Query Match 100.0%; Score 33; DB 7; Length 52;
Best Local Similarity 40.0%; Pred. No. 76;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|

Db 21 FQAGPRICLG 30

RESULT 4
US-11-096-568A-25378
; Sequence 25378, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25378
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(61)
; OTHER INFORMATION: Ceres Seq. ID no. 12589527

US-11-096-568A-25378

Query Match 100.0%; Score 33; DB 7; Length 61;
Best Local Similarity 40.0%; Pred. No. 87;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXCXG 10
|:|:|:|:|:
Db 3 FGGGLRCPVG 12

RESULT 5

US-11-087-099-10778

; Sequence 10778, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 39-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10778
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(71)
; OTHER INFORMATION: unsure at all Xaa locations

US-11-087-099-10778

Query Match 100.0%; Score 33; DB 7; Length 71;
Best Local Similarity 40.0%; Pred. No. 99;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXCXG 10
|:|:|:|:|:
Db 23 FKVGELPCRG 32

RESULT 6

US-11-116-881A-542

; Sequence 542, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.

US-11-116-881A

; SOFTWARE: PatentIn version 3.3
; NUMBER OF SEQ ID NOS: 2300
; SEQ ID NO 542
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

US-11-116-881A-542

; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 542
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

US-11-116-881A-542

Query Match 100.0%; Score 33; DB 7; Length 73;
Best Local Similarity 40.0%; Pred. No. 1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXCXG 10
|:|:|:|:|:
Db 6 FGGRRSCPG 15

RESULT 7

US-11-116-881A-546

; Sequence 546, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.

US-11-116-881A

; SOFTWARE: PatentIn version 3.3
; NUMBER OF SEQ ID NOS: 2300
; SEQ ID NO 546
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

US-11-116-881A-546

Query Match 100.0%; Score 33; DB 7; Length 73;
Best Local Similarity 40.0%; Pred. No. 1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXCXG 10
|:|:|:|:|:
Db 6 FGGRRSCPG 15

RESULT 8

US-10-467-657-8472

; Sequence 8472, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8472
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8472

Query Match 100.0%; Score 33; DB 6; Length 75;
Best Local Similarity 40.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
Db 53 FLFGLQTCRG 62
|::|::|::|

RESULT 9
US-10-453-372-494
; Sequence 494, Application US/10453372
; Publication No. US20060003232A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 03/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 03/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 03/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 494
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-494

Query Match 100.0%; Score 33; DB 6; Length 84;
Best Local Similarity 40.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
Db 51 FPQGSGRCLG 60
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RESULT 10
US-11-116-881A-548
; Sequence 548, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 548
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-548

Query Match 100.0%; Score 33; DB 7; Length 86;
Best Local Similarity 40.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
Db 19 FGSGRSCLG 28
|::|::|::|

RESULT 11
US-11-096-568A-25377
; Sequence 25377, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25377
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(99)
; OTHER INFORMATION: Ceres Seq. ID no. 12589526
US-11-096-568A-25377

Query Match 100.0%; Score 33; DB 7; Length 99;

Best Local Similarity 40.0%; Pred. No. 1.3e+02; Mismatches 6; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 41 FGGGLRFCVG 50

RESULT 12

US-11-116-881A-2299
; Sequence 2299, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2299
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Nicotiana Tabacum
US-11-116-881A-2299

Query Match 100.0%; Score 33; DB 7; Length 101;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 34 FGGRRSCPG 43

RESULT 13

US-11-072-512-3124
; Sequence 3124, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3124
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3124

Query Match 100.0%; Score 33; DB 7; Length 103;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 44 FSAGPNCIG 53

RESULT 14

US-11-096-568A-26958
; Sequence 26958, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26958
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(107)
; OTHER INFORMATION: Ceres Seq. ID no. 13636171
US-11-096-568A-26958

Query Match 100.0%; Score 33; DB 7; Length 107;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 40 FRKGRACSG 49

RESULT 15

US-10-821-234-1478
; Sequence 1478, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and Treatment of Preeclampsia

```

; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1478
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1478

```

```
Query Match      100.0%; Score 33; DB 6; Length 113;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```

RESULT 16
US-11-087-099-6613
; Sequence 6613, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6613
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-087-099-6613

```

Query Match 100.0%; Score 33; DB 7; Length 117;
Best Local Similarity 40.0%; Pred. NO. 1.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

RESULT 17
US-11-116-881A-464
; Sequence 464, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116, 881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17

Query Match 100.0%; Score 33; DB 7; Length 119;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels

```

; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 464
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; US-11-116-881A-464

      Query Match      100.0%; Score 33; DB 7; Length 118;
      Best Local Similarity 40.0%; Pred. No. 1.5e+02;
      Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy      1 FXXGXXXCXG 10
      ||::||::||
Db      51 FGSGRSCPG 60

```

RESULT 18
US-11-116-881A-460
; Sequence 460, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 460
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-460

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 52 FGSGRRSCPG 61

RESULT 19

US-11-072-512-2610
; Sequence 2610, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YORI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2610
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2610

Query Match 100.0%; Score 33; DB 7; Length 126;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|::|
Db 37 FSHGAPGCG 46

RESULT 20

US-11-166-609-14
; Sequence 14, Application US/11166609
; Publication No. US20060015968A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMNELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: 1148CR
; CURRENT APPLICATION NUMBER: US/11/166,609
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 10/412,000
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 09/670,153
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 14
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Zea mays
US-11-166-609-14

RESULT 19

US-11-166-609-15
; Sequence 15, Application US/11166609
; Publication No. US20060015968A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMNELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: 1148CR
; CURRENT APPLICATION NUMBER: US/11/166,609
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 10/412,000
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 09/670,153
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 15
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Zea mays
US-11-166-609-15

Query Match 100.0%; Score 33; DB 7; Length 128;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|::|
Db 68 FQAPRICLG 77

RESULT 22

US-11-116-881A-500
; Sequence 500, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368

RESULT 22

US-11-116-881A-500
; Sequence 500, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368

```

; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 500
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-500

Query Match      100.0%; Score 33; DB 7; Length 129;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXXGXXXCXG 10
Db      62 FSGRRSCPG 71

RESULT 23
US-11-116-881A-516
; Sequence 516, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 516
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-516

Query Match      100.0%; Score 33; DB 7; Length 129;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXXGXXXCXG 10
Db      103 FSGRRSCPG 112

RESULT 24
US-11-116-881A-540
; Sequence 540, Application US/11116881A

```

```

; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 540
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-540

Query Match      100.0%; Score 33; DB 7; Length 129;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXXGXXXCXG 10
Db      62 FSGRRSCPG 71

RESULT 25
US-11-143-980-68
; Sequence 68, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: He, Min
; APPLICANT: Hucul, John
; APPLICANT: Haltli, Bradley A.
; APPLICANT: Wagenaar, Melissa M.
; APPLICANT: Graziani, Edmund
; APPLICANT: Summers, Mia
; APPLICANT: Kulowski, Kerry
; APPLICANT: Pong, Kevin
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
; FILE REFERENCE: AM-101426US
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US 60/576,895
; PRIOR FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
; LENGTH: 134
; TYPE: PRT

```


; ORGANISM: Streptomyces sp.
US-11-143-980-88

Query Match 100.0%; Score 33; DB 7; Length 134;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 58 FDSGLDVCCG 67

RESULT 26

US-11-116-881A-456
; Sequence 456, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116.881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 456
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-456

Query Match 100.0%; Score 33; DB 7; Length 135;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 68 FPGRRSCPG 77

RESULT 27

US-11-116-881A-520
; Sequence 520, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116.881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451

; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 520
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-520

Query Match 100.0%; Score 33; DB 7; Length 137;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:|:|:|:|:
Db 71 FGVGRICPG 80

RESULT 28

US-11-116-881A-462
; Sequence 462, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116.881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 462
; LENGTH: 140

```
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-462

Query Match      100.0%; Score 33; DB 7; Length 140;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
   |:|:|:|:|
Db 73 FGSGRRSCPG 82

RESULT 29
US-11-084-508-22
; Sequence 22, Application US/11084508
; Publication No. US20050260737A1
; GENERAL INFORMATION:
; APPLICANT: Rahman, Raja Noor Zaliha Abd.
; APPLICANT: Salleh, Abu Bakar
; APPLICANT: Baeri, Mahiran
; APPLICANT: Hun, Chin John
; TITLE OF INVENTION: Novel Lipase Gene from Bacillus sphaericus 205Y
; FILE REFERENCE: KAN-101
; CURRENT APPLICATION NUMBER: US/11/084,508
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: MY 20040958
; PRIOR FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Moraxella sp.
US-11-084-508-22

Query Match      100.0%; Score 33; DB 7; Length 141;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
   |:|:|:|:|
Db 32 PFHGGGFCIG 41

RESULT 30
US-11-116-881A-448
; Sequence 448, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 510
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-510

Query Match      100.0%; Score 33; DB 7; Length 151;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
   |:|:|:|:|
Db 86 FGAGRRICPG 95

RESULT 32
US-11-096-568A-12468
; Sequence 12468, Application US/11096568A
```

```
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12468
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Triticum aestivum
; NAME/KEY: misc feature
; LOCATION: (1)..(155)
; OTHER INFORMATION: Ceres Seq. ID no. 14301815
US-11-096-568A-12468

Query Match      100.0%; Score 33; DB 7; Length 155;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXXGXXXCXG 10
Db      5 FPRGNRLCSG 14

RESULT 33
US-11-096-568A-14864
; Sequence 14864, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14864
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc feature
; LOCATION: (1)..(156)
; OTHER INFORMATION: Ceres Seq. ID no. 12340683
US-11-096-568A-14864

Query Match      100.0%; Score 33; DB 7; Length 156;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXXGXXXCXG 10
Db      90 FSCGRHSCVG 99

RESULT 34
US-11-096-568A-14863
; Sequence 14863, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14863
; LENGTH: 158
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; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc feature
; LOCATION: (1)..(158)
; OTHER INFORMATION: Ceres Seq. ID no. 12340682
US-11-096-568A-14863

Query Match      100.0%; Score 33; DB 7; Length 158;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXXGXXXCXG 10
Db      92 FSCGRHSCVG 101

RESULT 35
US-11-116-881A-486
; Sequence 486, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 486
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-486

Query Match      100.0%; Score 33; DB 7; Length 162;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXXGXXXCXG 10
Db      97 FGAGRRICPG 106

RESULT 36
US-11-116-881A-484
; Sequence 484, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
```

; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 484
; TYPE: PRT
; LENGTH: 164
; ORGANISM: Nicotiana tabacum
; NAME/KEY: VARIANT
; LOCATION: (27)..
; OTHER INFORMATION: Xaa = Leu, Pro, His, or Arg.
US-11-116-881A-484

Query Match 100.0%; Score 33; DB 7; Length 164;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 92 FGMGRRACPG 101

RESULT 37
US-11-116-881A-470
; Sequence 470, Application US/11/116,881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 484
; TYPE: PRT
; LENGTH: 164
; ORGANISM: Nicotiana tabacum
; NAME/KEY: VARIANT
; LOCATION: (27)..
; OTHER INFORMATION: Xaa = Leu, Pro, His, or Arg.
US-11-116-881A-484

; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-470

Query Match 100.0%; Score 33; DB 7; Length 175;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 108 FGSGRSFCPG 117

RESULT 38
US-11-120-308-106
; Sequence 106, Application US/11/120,308
; Publication No. US2006005277A1
; GENERAL INFORMATION:
; APPLICANT: Farnoud, Omolayo O.
; APPLICANT: Miao, Guo-Rua
; TITLE OF INVENTION: cDNAs Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/11/120,308
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/10/078,770
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 106
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (134)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (141)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (145)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (149)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (170)

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;
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (172)
US-11-120-308-106

Query Match      100.0%; Score 33; DB 7; Length 176;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
   |::|::|::|
Db 60 FINGPPCQG 69

RESULT 39
US-11-116-881A-522
; Sequence 522, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116.881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-01-25
; PRIOR FILING DATE: 2004-09-03
; PRIOR FILING DATE: 2004-04-29
; PRIOR FILING DATE: 2004-09-03
; PRIOR FILING DATE: 2004-09-17
; PRIOR FILING DATE: 2004-09-17
; PRIOR FILING DATE: 2003-09-18
; PRIOR FILING DATE: 2003-09-18
; PRIOR FILING DATE: 2003-07-08
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 522
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

US-11-116-881A-502
; Sequence 502, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116.881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-01-25
; PRIOR FILING DATE: 2004-09-03
; PRIOR FILING DATE: 2004-04-29
; PRIOR FILING DATE: 2004-09-03
; PRIOR FILING DATE: 2004-09-17
; PRIOR FILING DATE: 2004-09-17
; PRIOR FILING DATE: 2003-09-18
; PRIOR FILING DATE: 2003-09-18
; PRIOR FILING DATE: 2003-07-08
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 522
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

US-11-116-881A-522

Query Match      100.0%; Score 33; DB 7; Length 176;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
   |::|::|::|
Db 107 FGGRRSCPG 116

RESULT 40
US-11-116-881A-502
; Sequence 502, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116.881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-01-25
; PRIOR FILING DATE: 2004-09-03
; PRIOR FILING DATE: 2004-04-29
; PRIOR FILING DATE: 2004-09-03
; PRIOR FILING DATE: 2004-09-17
; PRIOR FILING DATE: 2004-09-17
; PRIOR FILING DATE: 2003-09-18
; PRIOR FILING DATE: 2003-09-18
; PRIOR FILING DATE: 2003-07-08
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 522
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

US-11-116-881A-522

Query Match      100.0%; Score 33; DB 7; Length 176;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
   |::|::|::|
Db 107 FGGRRSCPG 116

RESULT 41
US-10-467-657-1228
; Sequence 1228, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1228
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-1228

Query Match      100.0%; Score 33; DB 6; Length 185;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
   |::|::|::|
Db 24 FCCGREGCG 33

RESULT 42
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US-11-116-881A-458
; Sequence 458, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-01-25
; PRIOR FILING DATE: 2004-09-03
; PRIOR FILING DATE: 2004-09-17
; PRIOR FILING DATE: 2003-09-18
; PRIOR FILING DATE: 2003-07-08
; PRIOR FILING DATE: 2003-07-08
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 458
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-458

Query Match 100.0%; Score 33; DB 7; Length 187;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|
DB 120 FGSGRRSCPG 129

RESULT 43
US-11-096-568A-23881
; Sequence 23881, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23881
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(194)
; OTHER INFORMATION: Ceres Seq. ID no. 12416120
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (131)..(131)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-23881

Query Match 100.0%; Score 33; DB 7; Length 194;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGXGXXCXG 10
|::|::|::|
DB 125 FGAGRRXCAG 134
RESULT 44
US-11-096-568A-18243
; Sequence 18243, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18243
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(197)
; OTHER INFORMATION: Ceres Seq. ID no. 12363892
US-11-096-568A-18243

Query Match 100.0%; Score 33; DB 7; Length 197;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|
DB 154 FGAGRRXCAG 163

RESULT 45
US-09-995-493-12
; Sequence 12, Application US/09995493
; Publication No. US20060035293A1
; GENERAL INFORMATION:
; APPLICANT: Handfield, Martin
; APPLICANT: Hillman, Jeffrey
; APPLICANT: Progulskie-Fox, Ann
; TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans Antigens for
; FILE REFERENCE: MBH01-662
; CURRENT APPLICATION NUMBER: US/09/995,493
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Actinobacillus actinomycetemcomitans
US-09-995-493-12

Query Match 100.0%; Score 33; DB 5; Length 199;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|
DB 102 PEGAGGICYG 111

RESULT 46
US-11-087-099-7405

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; Sequence 7405, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7405
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Populus x canescens
; US-11-087-099-7405

Query Match      100.0%; Score 33; DB 7; Length 208;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXGXGXXCXG 10
      |::|::|::|
Db      136 FGAGRRMCPG 145

RESULT 47
US-11-087-099-11148
; Sequence 11148, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11148
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Phanerochaete chrysosporium
; US-11-087-099-11148

Query Match      100.0%; Score 33; DB 7; Length 208;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXGXGXXCXG 10
      |::|::|::|
Db      143 FNAGPRICLG 152

RESULT 48
US-11-096-568A-23880
; Sequence 23880, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23880
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(210)
; OTHER INFORMATION: Ceres Seq. ID no. 12416119
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
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; OTHER INFORMATION: Xaa is any aa, unknown or other
; US-11-096-568A-23880

Query Match      100.0%; Score 33; DB 7; Length 210;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXGXGXXCXG 10
      |::|::|::|
Db      141 FGAGREXCAG 150

RESULT 49
US-11-087-099-2635
; Sequence 2635, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2635
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Candida tropicalis
; US-11-087-099-2635

Query Match      100.0%; Score 33; DB 7; Length 213;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXGXGXXCXG 10
      |::|::|::|
Db      153 FNGGPRICLG 162

RESULT 50
US-11-087-099-11719
; Sequence 11719, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11719
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Candida maltosa
; US-11-087-099-11719

Query Match      100.0%; Score 33; DB 7; Length 213;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXGXGXXCXG 10
      |::|::|::|
Db      153 FNGGPRICLG 162

Search completed: March 8, 2006, 11:28:48
Job time : 24 secs
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Result No.	Query			ID	Description.
	Score	Match	Length		
1	33	100.0	10	1	US-07-912-900-1
2	33	100.0	10	1	US-08-285-309-1
3	33	100.0	10	1	US-08-502-046-1
4	33	100.0	10	2	US-08-948-564-21
5	33	100.0	10	2	US-09-304-615-129
6	33	100.0	10	2	US-10-054-988-129
7	33	100.0	11	1	US-07-912-900-13
8	33	100.0	11	1	US-07-912-900-14
9	33	100.0	11	1	US-07-912-900-15
10	33	100.0	11	1	US-08-285-309-13
11	33	100.0	11	1	US-08-285-309-14
12	33	100.0	11	1	US-08-285-309-15
13	33	100.0	11	1	US-08-313-075A-12
14	33	100.0	11	1	US-08-313-075A-13
15	33	100.0	11	1	US-08-313-075A-14
16	33	100.0	11	1	US-08-502-046-13
17	33	100.0	11	1	US-08-502-046-14
18	33	100.0	11	1	US-08-502-046-15
19	33	100.0	11	2	US-09-459-302A-3
20	33	100.0	13	2	US-08-948-564-20
21	33	100.0	14	1	US-08-845-161A-10
22	33	100.0	14	1	US-08-845-161A-19
23	33	100.0	14	1	US-08-845-161A-20
24	33	100.0	14	1	US-08-845-161A-21
25	33	100.0	14	1	US-08-845-161A-22
26	33	100.0	14	1	US-08-845-161A-23
27	33	100.0	14	1	US-08-845-161A-24

ALIGNMENTS

RESULT 1
US-07-912-900-1
; Sequence 1, Application US/07912900
; Patent No. 5349125
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/912,900
; FILING DATE: 19920713
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-912-900-1
Query Match 100.0%; Score 33; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXGXXXCXG 10
| | | | |
Db 1 FXXGXXXCXG 10
RESULT 2
US-08-285-309-1
; Sequence 1, Application US/08285309
; Patent No. 5569832
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; TITLE OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,309
; FILING DATE: 03-AUG-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-285-309-1
Query Match 100.0%; Score 33; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXGXXXCXG 10
| | | | |
Db 1 FXXGXXXCXG 10
RESULT 3
US-08-502-046-1
; Sequence 1, Application US/08502046
; Patent No. 5861487
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; TITLE OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,046
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 800
; TITLE OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29

```

; FILING DATE: 03-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-502-046-1
;
Query Match 100.0%; Score 33; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 FXGXGXXCXG 10
;
DB 1 FXGXGXXCXG 10
;
;
RESULT 4
US-08-948-564-21
; Sequence 21, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminsky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512a Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-948-564-21
;
Query Match 100.0%; Score 33; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 7
US-07-912-900-13
; Sequence 13, Application US/07912900
; Patent No. 5349125
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/912,900
; FILING DATE: 19920713
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-912-900-13
Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXGXXXCXG 10
|:|:|:|:
Db 2 FGAGRGCGP 11
RESULT 8
US-07-912-900-14
; Sequence 14, Application US/07912900
; Patent No. 5349125
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City

STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,900
FILING DATE: 19920713
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-912-900-14
Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXGXXXCXG 10
|:|:|:|:
Db 2 FGAGRGCGP 11
RESULT 9
US-07-912-900-15
; Sequence 15, Application US/07912900
; Patent No. 5349125
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/912,900
; FILING DATE: 19920713
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-912-900-15

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFXGXXCXG 10
|::|::|::|
Db 2 FGSRRICPG 11

RESULT 10
US-08-285-309-13
Sequence 13, Application US/08285309
Patent No. 5569832
GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filippa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3.5'-
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,309
FILING DATE: 03-AUG-1994
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-285-309-13

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFXGXXCXG 10
|::|::|::|
Db 2 FGSRRICPG 11

RESULT 11
US-08-285-309-14
Sequence 14, Application US/08285309
Patent No. 5569832
GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filippa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3.5'-
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,309
FILING DATE: 03-AUG-1994
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-285-309-14

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFXGXXCXG 10
|::|::|::|
Db 2 FGSRRICPG 11

RESULT 12
US-08-285-309-15
Sequence 15, Application US/08285309
Patent No. 5569832
GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filippa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3.5'-
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza

CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,309
FILING DATE: 03-AUG-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633Z
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-285-309-15

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXCXG 10
|::|::|::|:
Db 2 FGSGRRICPG 11

RESULT 13
US-08-313-075A-12
Sequence 12, Application US/08313075A
Patent No. 5639870
GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,075A
FILING DATE: 30-NOV-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 1538/92
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 6698/93
FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9433
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-075A-12

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXCXG 10
|::|::|::|:
Db 2 FGAGRRGCPG 11

RESULT 14
US-08-313-075A-13
Sequence 13, Application US/08313075A
Patent No. 5639870
GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,075A
FILING DATE: 30-NOV-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 1538/92
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 6698/93
FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9433
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-075A-13

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|
Db 2 FGAGRGRCGP 11

RESULT 15

US-08-313-075A-14

; Sequence 14, Application US/08313075A
; Patent No. 5639870
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Tanaka, Yoshikazu
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,075A
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 1538/92
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 6698/93
; FILING DATE: 07-JAN-1993

; APPLICATION NUMBER: AU PCT/AU93/00127
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9433

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-313-075A-14

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|
Db 2 FGAGRGRCGP 11

RESULT 16

US-08-502-046-13

; Sequence 13, Application US/08502046
; Patent No. 5861487
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; TITLE OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,046
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,309
; FILING DATE: 03-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-502-046-13

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|
Db 2 FGAGRGRCGP 11

RESULT 17

US-08-502-046-14

; Sequence 14, Application US/08502046
; Patent No. 5861487
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu

```

; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; NUMBER OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,046
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,309
; FILING DATE: 03-AUG-1994
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-502-046-14

```

```

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwin C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,046
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,309
; FILING DATE: 03-AUG-1994
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-502-046-15

```

```

Query Match 100.0%; Score 33; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

; APPLICANT: BOUNG-JUN, OH
; APPLICANT: MOON, KYUNG KO
; APPLICANT: YOUNG, SOON KIM
; TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
; FILE REFERENCE: 10324/P6443USO
; CURRENT APPLICATION NUMBER: US/09/499,302A
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: heme-binding domain
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: variable or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: variable or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: variable or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: variable or unknown amino acid
; US-09-499-302A-3

```

```

; Sequence 3, Application US/09499302A
; Patent No. 6369212
; GENERAL INFORMATION:
; APPLICANT: BOUNG-JUN, OH
; APPLICANT: MOON, KYUNG KO
; APPLICANT: YOUNG, SOON KIM
; TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
; FILE REFERENCE: 10324/P6443USO
; CURRENT APPLICATION NUMBER: US/09/499,302A
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: heme-binding domain
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: variable or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: variable or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: variable or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: variable or unknown amino acid
; US-09-499-302A-3

```

```

Query Match 100.0%; Score 33; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```


Qy 1 FXGXGXXCXG 10
|:|||||
Db 2 FGXGXXCXG 11

RESULT 20

US-08-948-564-20
; Sequence 20, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminezy, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: NO. 6121512 Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-948-564-20

Query Match 100.0%; Score 33; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|||||
Db 4 FGXGXXCXG 13

RESULT 21

US-08-845-161A-10
; Sequence 10, Application US/08845161A
; Patent No. 5976850
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
; APPLICANT: Rose, Kenneth A.
; APPLICANT: Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 5976850th Glebe Rd. 8th floor
; CITY: Arlington

; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,161A
; FILING DATE: 21-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 604-408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-845-161A-10

Query Match 100.0%; Score 33; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|||||
Db 1 FXGXGXXCXG 10

RESULT 22

US-08-845-161A-19
; Sequence 19, Application US/08845161A
; Patent No. 5976850
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
; APPLICANT: Rose, Kenneth A.
; APPLICANT: Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 5976850th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,161A
; FILING DATE: 21-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995

```
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9421093.7
;; FILING DATE: 19-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mary J.
;; REGISTRATION NUMBER: 32,955
;; REFERENCE/DOCKET NUMBER: 604-408
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-816-4000
;; TELEFAX: 703-816-4100
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-845-161A-19

Query Match 100.0%; Score 33; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
DB 1 FGLGTSKCPG 10

RESULT 23
US-08-845-161A-20
; Sequence 20, Application US/08845161A
; Patent No. 5976850
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
; APPLICANT: Rose, Kenneth A.
; APPLICANT: Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 5976850th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,161A
; FILING DATE: 21-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 604-408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
```

```
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-845-161A-20

Query Match 100.0%; Score 33; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
DB 1 FGSGATICPG 10

RESULT 24
US-08-845-161A-21
; Sequence 21, Application US/08845161A
; Patent No. 5976850
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
; APPLICANT: Rose, Kenneth A.
; APPLICANT: Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 5976850th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,161A
; FILING DATE: 21-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 604-408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-845-161A-21

Query Match 100.0%; Score 33; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
DB 1 FGAGPRSCVG 10

RESULT 25
US-08-845-161A-22
```

APPLICANT: SCAPULON, GENIEVIEW
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5976850th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA

```

; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 604-408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-845-161A-24

Query Match 100.0%; Score 33; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|:::|:|
Db 1 FGWGVRCQLG 10

RESULT 28
US-08-845-161A-25
; Sequence 25, Application US/08845161A
; Patent No. 5976850
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
; APPLICANT: Rose, Kenneth A.
; APPLICANT: Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 5976850th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,161A
; FILING DATE: 21-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 604-408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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US-08-845-161A-25

Query Match 100.0%; Score 33; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|:::|:|
Db 1 FGWGVRCQLG 10

RESULT 29
US-09-270-751-10
; Sequence 10, Application US/09270751
; Patent No. 6184350
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
; APPLICANT: Rose, Kenneth A.
; APPLICANT: Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 6184350th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,751
; FILING DATE: 17-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 604-408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-270-751-10

Query Match 100.0%; Score 33; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|:::|:|
Db 1 FXGXGXXCXG 10

RESULT 30
US-09-270-751-19
; Sequence 19, Application US/09270751
; Patent No. 6184350

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GENERAL INFORMATION:
APPLICANT: Lathe, Richard
Rose, Kenneth A.
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 No. 6184350th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,751
FILING DATE: 17-Apr-2000
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-270-751-19

Query Match 100.0%; Score 33; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 1 FGLGTSKCPG 10

RESULT 31
US-09-270-751-20
Sequence 20, Application US/09270751
Patent No. 6184350
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
Rose, Kenneth A.
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 No. 6184350th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,751
FILING DATE: 17-Apr-2000
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-270-751-20

Query Match 100.0%; Score 33; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 1 FGSGATICPG 10

RESULT 32
US-09-270-751-21
Sequence 21, Application US/09270751
Patent No. 6184350
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
Rose, Kenneth A.
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 No. 6184350th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,751
FILING DATE: 17-Apr-2000
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.

```
;
;   REGISTRATION NUMBER: 32,955
;   REFERENCE/DOCKET NUMBER: 604-408
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-816-4000
;   TELEFAX: 703-816-4100
;   INFORMATION FOR SEQ ID NO: 21:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 14 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-270-751-21

Query Match      100.0%; Score 33; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXGXGXXCXG 10
|::|::|::|
Db      1 FGAGPRSCVG 10

RESULT 33
US-09-270-751-22
; Sequence 22, Application US/09270751
; Patent No. 6184350
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard A.
; Rose, Kenneth A.
; Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 6184350th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,751
; FILING DATE: 17-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 604-408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-270-751-22
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Query Match      100.0%; Score 33; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXGXGXXCXG 10
|::|::|::|
Db      1 FGAGPRSCVG 10

RESULT 34
US-09-270-751-23
; Sequence 23, Application US/09270751
; Patent No. 6184350
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard A.
; Rose, Kenneth A.
; Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 6184350th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,751
; FILING DATE: 17-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02465
; FILING DATE: 18-OCT-1995
; APPLICATION NUMBER: GB 9421093.7
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 604-408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-270-751-23

Query Match      100.0%; Score 33; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FXGXGXXCXG 10
|::|::|::|
Db      1 FGCGARVCLG 10

RESULT 35
US-09-270-751-24
; Sequence 24, Application US/09270751
; Patent No. 6184350
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard A.
```

;; Rose, Kenneth A.
;; Stapleton, Genevieve
;; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
;; SEQUENCES CODING THEREFOR AND USED THEREOF
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHVE P.C.
;; STREET: 1100 No. 6184350th Glebe Rd. 8th floor
;; CITY: Arlington
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22201-4741
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/270,751
;; FILING DATE: 17-Apr-2000
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB95/02465
;; FILING DATE: 18-OCT-1995
;; APPLICATION NUMBER: GB 9421093.7
;; FILING DATE: 19-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mary J.
;; REGISTRATION NUMBER: 32,955
;; REFERENCE/DOCKET NUMBER: 604-408
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-816-4000
;; TELEFAX: 703-816-4100
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-270-751-24

Query Match 100.0%; Score 33; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 1 FGWGVROCLG 10

RESULT 36
US-09-270-751-25
; Sequence 25, Application US/09270751
; Patent No. 6184350
; GENERAL INFORMATION:
; APPLICANT: Lathe, Richard
; Rose, Kenneth A.
; Stapleton, Genevieve
; TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
; SEQUENCES CODING THEREFOR AND USED THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 6184350th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/270,751
;; FILING DATE: 17-Apr-2000
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB95/02465
;; FILING DATE: 18-OCT-1995
;; APPLICATION NUMBER: GB 9421093.7
;; FILING DATE: 19-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mary J.
;; REGISTRATION NUMBER: 32,955
;; REFERENCE/DOCKET NUMBER: 604-408
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-816-4000
;; TELEFAX: 703-816-4100
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-270-751-25

Query Match 100.0%; Score 33; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 1 FGWGVROCLG 10

RESULT 37
5204096-22
; Patent No. 5204096
; APPLICANT: NEURATH, ALEXANDER R.; KENT, B.H.
; TITLE OF INVENTION: PRE-S GENE CODED PEPTIDE HEPATITIS B
; IMMUNOGENS, VACCINES, DIAGNOSTICS, AND SYNTHETIC LIPID VESICLE
; CARRIERS
; NUMBER OF SEQUENCES: 36
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/338,028
; FILING DATE: 14-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 698,499
; FILING DATE: 05-FEB-1985
; APPLICATION NUMBER: 587,090
; FILING DATE: 07-MAR-1984
; SEQ ID NO: 22:
; LENGTH: 15
5204096-22

Query Match 100.0%; Score 33; DB 6; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 4 FLGGTTVCLG 13

RESULT 38
US-09-471-276-1257
; Sequence 1257, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.

APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 682072
FILE REFERENCE: GENSET.025CP1
CURRENT APPLICATION NUMBER: US/09/471.276
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 09/069,047
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: Patent.pm
SEQ ID NO 1257
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -14..-1
US-09-471-276-1257

Query Match 100.0%; Score 33; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|:|:|:|:|:
Db 4 PFGNSPCG 13

RESULT 39
US-102-863-2
Sequence 2, Application US/08102863
Patent No. 546590
GENERAL INFORMATION:
APPLICANT: SARIASLANI, SIMA
TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: EXPRESSION OF P450SOY
TITLE OF INVENTION: AND FERREDOXIN-SOY IN
TITLE OF INVENTION: STREPTOMYCES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,863
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/807,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-7342
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-102-863-2

Query Match 100.0%; Score 33; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|:|:|:|:|:
Db 5 FGFVHQCLG 14

RESULT 40
PCT-US92-10885-2
Sequence 2, Application PC/TUS9210885
GENERAL INFORMATION:
APPLICANT: SARIASLANI, SIMA
TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: EXPRESSION OF P450SOY
TITLE OF INVENTION: AND FERREDOXIN-SOY IN
TITLE OF INVENTION: STREPTOMYCES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10885
FILING DATE: 19921216
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9000-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-7342
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US92-10885-2

Query Match 100.0%; Score 33; DB 4; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|:|:|:|:|:
Db 5 FGFVHQCLG 14

RESULT 41
US-08-484-135-27
Sequence 27, Application US/08484135
Patent No. 5767078


```

; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frank S. DiGiglio
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A..
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-135-27

Query Match 100.0%; Score 33; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 8 FPGTWDCTG 17

RESULT 42
US-08-484-635-208
; Sequence 208, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-635-208

Query Match 100.0%; Score 33; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 8 FPGTWDCTG 17

RESULT 43
US-08-484-631-208
; Sequence 208, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043

```

;; INFORMATION FOR SEQ ID NO: 208:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 20 amino acids

;; TYPE: amino acid

;; STRANDEDNESS:

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

US-08-484-631-208

Query Match 100.0%; Score 33; DB 1; Length 20;

Best Local Similarity 40.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10

Db 8 FPGTWDCTG 17

RESULT 44

US-08-827-570-208

;; Sequence 208, Application US/08827570

;; Patent No. 5986047

;; GENERAL INFORMATION:

;; APPLICANT: Wrighton, Nicholas C.

;; APPLICANT: Dower, William J.

;; APPLICANT: Chang, Ray S.

;; APPLICANT: Kashyap, Arun K.

;; APPLICANT: Jolliffe, Linda K.

;; APPLICANT: Johnson, Dana

;; APPLICANT: Mulcahy, Linda

;; TITLE OF INVENTION: Compounds and Peptides That Bind to the

;; TITLE OF INVENTION: Erythropoietin Receptor

;; NUMBER OF SEQUENCES: 259

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew

;; STREET: One Market Plaza, Steuart Street Tower

;; CITY: San Francisco

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94105-1492

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/827,570

;; FILING DATE:

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/484,635

;; FILING DATE: 07-JUN-1995

;; APPLICATION NUMBER: US 08/155,940

;; FILING DATE: 19-NOV-1993

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Garrett-Wackowski, Eugenia

;; REGISTRATION NUMBER: 37,330

;; REFERENCE/DOCKET NUMBER: 16528A-43-1-1

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 543-9600

;; TELEFAX: (415) 543-5043

;; INFORMATION FOR SEQ ID NO: 208:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 20 amino acids

;; TYPE: amino acid

;; STRANDEDNESS:

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

US-08-827-570-208

Query Match

Best Local Similarity 100.0%; Score 33; DB 1; Length 20;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10

Db 8 FPGTWDCTG 17

RESULT 45

US-08-724-466B-6

;; Sequence 6, Application US/08724466B

;; Patent No. 6063606

;; GENERAL INFORMATION:

;; APPLICANT: Petkovich, P. Martin, White, Jay A.,

;; APPLICANT: Beckett, Barbara R., Jones, Glenville

;; TITLE OF INVENTION: Retinoid Metabolizing Protein

;; NUMBER OF SEQUENCES: 30

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Blake, Cassels & Graydon

;; STREET: Box 25, Commerce Court West

;; CITY: Toronto

;; ZIP: M5L 1A9

;; COUNTRY: Canada

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

;; COMPUTER: COMPAQ, IBM PC compatible

;; OPERATING SYSTEM: MS-DOS 5.1

;; SOFTWARE: WORD PERFECT

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/724,466B

;; FILING DATE: October 1, 1996

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/667,546

;; FILING DATE: June 21, 1996

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hunt, John C.

;; REGISTRATION NUMBER: 36,424

;; REFERENCE/DOCKET NUMBER: 50767/00004

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (416) 863-4344

;; TELEFAX: (416) 863-2653

;; INFORMATION FOR SEQ ID NO: 6:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 20 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

US-08-724-466B-6

Query Match 100.0%; Score 33; DB 2; Length 20;

Best Local Similarity 40.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10

Db 2 FGGGRLCPG 11

RESULT 46

US-08-724-466B-7

;; Sequence 7, Application US/08724466B

;; Patent No. 6063606

;; GENERAL INFORMATION:

;; APPLICANT: Petkovich, P. Martin, White, Jay A.,

;; APPLICANT: Beckett, Barbara R., Jones, Glenville

;; TITLE OF INVENTION: Retinoid Metabolizing Protein

;; NUMBER OF SEQUENCES: 30

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Blake, Cassels & Graydon

;; STREET: Box 25, Commerce Court West

;; CITY: Toronto

;; ZIP: M5L 1A9

;; COUNTRY: Canada

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-724-466B-7

Query Match 100.0%; Score 33; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|::|
Db 2 FSGGARNCIG 11

RESULT 47
US-08-724-466B-8
Sequence 8, Application US/08724466B
Patent No. 6063606
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-724-466B-8

Query Match 100.0%; Score 33; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|::|
Db 2 FSGGARNCIG 11

RESULT 48
US-08-724-466B-9
Sequence 9, Application US/08724466B
Patent No. 6063606
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-724-466B-9

Query Match 100.0%; Score 33; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
|::|::|::|::|
Db 2 FSGGARNCIG 11

RESULT 49
US-08-724-466B-10
Sequence 10, Application US/08724466B
Patent No. 6063606
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto

```

; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-724-466B-10

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```

Query Match 100.0%; Score 33; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 FXGXXXXXG 10
Db 2 FSGGRNCIG 11

```

```

RESULT 50
US-08-882-164D-6
; Sequence 6, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653

```

```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-882-164D-6
Query Match 100.0%; Score 33; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXGXXXXXG 10
Db 2 FSGGRNCIG 11
Search completed: March 8, 2006, 11:25:27
Job time : 49 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 8, 2006, 11:20:19 ; Search time 38 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-10-751-235-14

Perfect score: 33

Sequence: 1 FXGXGXXCXG 10

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	29	2 A56591	E75 steroid recept
2	33	100.0	35	2 A82520	hypothetical prote
3	33	100.0	47	2 I48943	cellular disintegr
4	33	100.0	50	2 D72804	gp38 protein - Myc
5	33	100.0	63	2 S09643	probable cytochrom
6	33	100.0	66	2 A83575	hypothetical prote
7	33	100.0	70	2 T06525	cytochrome P450 ho
8	33	100.0	71	2 D81003	hypothetical prote
9	33	100.0	71	2 D82025	probable integral
10	33	100.0	74	2 T17791	hypothetical prote
11	33	100.0	78	2 T01646	apoptotic cell dea
12	33	100.0	80	2 S38926	hypothetical prote
13	33	100.0	87	2 T17723	hypothetical prote
14	33	100.0	89	2 T06524	probable cytochrom
15	33	100.0	96	2 AE2692	hypothetical prote
16	33	100.0	103	2 A75635	cytochrome P450-re
17	33	100.0	112	2 B82914	hypothetical prote
18	33	100.0	113	2 A54337	apoptotic cell dea
19	33	100.0	113	2 C54437	apoptotic cell dea
20	33	100.0	113	2 T149285	defender against a
21	33	100.0	114	2 T03016	probable apoptotic
22	33	100.0	115	2 S71269	apoptotic cell dea
23	33	100.0	115	2 F86446	probable defender
24	33	100.0	119	2 T17016	defender against c
25	33	100.0	119	2 T39694	hypothetical prote
26	33	100.0	119	2 H87152	hypothetical prote
27	33	100.0	122	2 T39039	probable oligosacc
28	33	100.0	122	2 T38989	hypothetical prote
29	33	100.0	124	2 T05467	hypothetical prote

30	33	100.0	126	2 I46935	aldehyde dehydroge
31	33	100.0	132	2 T28875	hypothetical prote
32	33	100.0	133	2 S61662	dolichyl-diphospho
33	33	100.0	136	2 F69870	general stress pro
34	33	100.0	137	2 S22388	phospholipase A2 (
35	33	100.0	137	2 A95297	hypothetical prote
36	33	100.0	139	2 G85060	hypothetical prote
37	33	100.0	139	2 E85060	hypothetical prote
38	33	100.0	141	2 T05465	hypothetical prote
39	33	100.0	141	2 H85060	hypothetical prote
40	33	100.0	141	2 T26567	hypothetical prote
41	33	100.0	142	2 T36312	hypothetical prote
42	33	100.0	143	2 T05466	hypothetical prote
43	33	100.0	144	2 PC4428	cytochrome P450 4C
44	33	100.0	145	2 S20227	reverse transcript
45	33	100.0	147	2 S36442	PilB-related prote
46	33	100.0	148	2 G82223	hypothetical prote
47	33	100.0	157	2 S30389	defender against c
48	33	100.0	160	2 F84769	cytochrome P450 mo
49	33	100.0	162	2 PC4262	cytochrome P450 PB
50	33	100.0	169	2 I55299	hypothetical 19.4K
51	33	100.0	173	2 S20689	thioredoxin peroxi
52	33	100.0	175	2 C81349	probable fibrial
53	33	100.0	176	2 F96824	hypothetical prote
54	33	100.0	178	2 AF0544	TATA-binding trans
55	33	100.0	181	2 D69084	TATA-binding trans
56	33	100.0	183	2 C64363	transcription init
57	33	100.0	183	2 E69296	TATA-binding trans
58	33	100.0	186	2 T44922	TATA box binding p
59	33	100.0	186	2 T08255	transcription init
60	33	100.0	186	2 A84375	transcription init
61	33	100.0	186	2 T08331	TATA-binding trans
62	33	100.0	189	2 S30172	mercury-binding pr
63	33	100.0	190	2 JC4514	TATA-binding prote
64	33	100.0	191	2 T47230	transcription fact
65	33	100.0	191	2 A54275	TATA-binding prote
66	33	100.0	191	2 E75072	transcription init
67	33	100.0	191	2 D71093	probable TATA-bind
68	33	100.0	200	1 TWPO2D	transcription init
69	33	100.0	200	2 S61088	transcription init
70	33	100.0	200	2 S21140	transcription init
71	33	100.0	200	2 S10946	transcription init
72	33	100.0	200	2 S10945	transcription init
73	33	100.0	201	2 S30216	transcription init
74	33	100.0	205	2 T27278	hypothetical prote
75	33	100.0	209	2 B95083	thiamine-phosphate
76	33	100.0	209	2 F97950	probable holocyto
77	33	100.0	213	2 E64030	transcription init
78	33	100.0	215	2 T03386	hypothetical prote
79	33	100.0	219	2 T08330	L1 protein - human
80	33	100.0	220	2 S48781	L1 protein - human
81	33	100.0	221	2 S48782	L1 protein - human
82	33	100.0	221	2 G83604	conserved hypotet
83	33	100.0	222	2 S48786	L1 protein - human
84	33	100.0	222	2 S48786	cobalamin biosynth
85	33	100.0	224	2 S37740	transcription fact
86	33	100.0	224	2 S48779	L1 protein - human
87	33	100.0	224	2 S48784	L1 protein - human
88	33	100.0	225	2 S48780	L1 protein - human
89	33	100.0	226	1 JQ1570	major surface anti
90	33	100.0	226	1 JQ1571	major surface anti
91	33	100.0	226	1 JQ1573	major surface anti
92	33	100.0	226	1 JQ1574	major surface anti
93	33	100.0	226	1 JQ1576	major surface anti
94	33	100.0	226	1 JQ1577	major surface anti
95	33	100.0	226	1 JQ1578	major surface anti
96	33	100.0	226	1 JQ1579	major surface anti
97	33	100.0	226	1 JQ1580	major surface anti
98	33	100.0	226	1 JQ1581	major surface anti
99	33	100.0	226	1 JQ1581	major surface anti
100	33	100.0	226	1 SAVLAR	major surface anti

ALIGNMENTS

RESULT 1

A56591
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: A56591
R;Segraves, W.A.; Woldin, C.
Proc. Natl. Acad. Sci. U.S.A. 91, 91-97, 1994
A;Title: The E75 gene of Manduca sexta and comparison with its Drosophila homolog.
A;Reference number: A56591; MUID:93250864; PMID:8485520
A;Accession: A56591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-29 <SEG>
A;Cross-references: UNIPROT:Q08893; UNIPARC:UPI000016BFF9; GB:S60782; NID:G385887; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:132107, NCBIP:132113)
C;Keywords: steroid hormone receptor

Query Match 100.0%; Score 33; DB 2; Length 29;
Best Local Similarity 40.0%; Pred. No. 89;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 18 FHYGVHSCEG 27

RESULT 2

A82520
hypothetical protein XF2749 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82520
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82520
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-35 <SIM>
A;Cross-references: UNIPROT:Q9P9X1; UNIPARC:UPI00000C2B3B; GB:AE004081; GB:AE003849; NID:
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshakoko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2749

Query Match 100.0%; Score 33; DB 2; Length 35;
Best Local Similarity 40.0%; Pred. No. 1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 5 FDAGAAICVG 14

RESULT 3

I48943
cellular disintegrin-related protein 16-2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Oct-2004
C;Accession: I48943
R;Westkamp, G.; Blobel, C.P.
Proc. Natl. Acad. Sci. U.S.A. 91, 2748-2751, 1994
A;Title: A new family of cellular proteins related to snake venom disintegrins.
A;Reference number: A53476; MUID:94195820; PMID:8146185
A;Accession: I48943
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-47 <RES>
A;Cross-references: UNIPROT:Q61072; UNIPARC:UPI000016CAB9; EMBL:U06145; NID:G487138; PID:
I48943

Query Match 100.0%; Score 33; DB 2; Length 47;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 35 FLPGSMCRG 44

RESULT 4

D72804
gp38 protein - Mycobacterium phage D29
C;Species: Mycobacterium phage D29
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: D72804
R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.
J. Mol. Biol. 279, 143-164, 1998
A;Title: Genome structure of mycobacteriophage D29: Implications for phage evolution.
A;Reference number: A72800; MUID:98300335; PMID:9636706
A;Accession: D72804
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <FOR>
A;Cross-references: UNIPROT:O64229; UNIPARC:UPI000013856F; GB:AF022214; NID:G3172250; PT:
C;Genetics:
A;Gene: 38

Query Match 100.0%; Score 33; DB 2; Length 50;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 13 FALGLTACDG 22

RESULT 5

S09643
probable cytochrome P450 - Neurospora crassa (fragment)
C;Species: Neurospora crassa
C;Date: 21-Nov-1993 #sequence_revision 17-Apr-1998 #text_change 05-Oct-2004
C;Accession: S09643
R;Attar, R.M.; Grotewold, E.; Taccioli, G.E.; Aisenberg, G.O.; Torres, H.N.; Judewicz, N
Nucleic Acids Res. 17, 7535-7536, 1989
A;Title: A cycloheximide-inducible gene of Neurospora crassa belongs to the cytochrome P
A;Reference number: S09643; MUID:90016828; PMID:2529480
A;Accession: S09643
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-63 <ATT>
A;Cross-references: UNIPARC:UPI000017A254; EMBL:X15033
C;Genetics:
A;Gene: CYP54

A;Introns: 11/2
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein
F;8/Binding site: heme iron (Cys) (axial ligand) #status predicted

```
Query Match      100.0%; Score 33; DB 2; Length 63;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
   |||::|||
Db 1 FGYGRHACPG 10

RESULT 6
A83575
hypothetical protein PA0553 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83575
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
gen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-66 <STO>
A;Cross-references: UNIPROT:Q915Y3; UNIPARC:UPI000000C50AF; GB:AE004492; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0553

Query Match      100.0%; Score 33; DB 2; Length 66;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
   |||::|||
Db 11 FCLGLAACSG 20

RESULT 7
T06525
cytochrome P450 homolog - garden pea (fragment)
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06525
R;Frank, M.R.; Deyneka, J.M.; Schuler, M.A.
Plant Physiol. 110, 1035-1046, 1996
A;Title: Cloning of wound-induced cytochrome P450 mono-oxygenases expressed in pea.
A;Reference number: Z15734; MUID:96417083; PMID:8819874
A;Accession: T06525
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-70 <FRA>
A;Cross-references: UNIPROT:Q40986; UNIPARC:UPI0000009CF11; EMBL:U29335; NID:g894156; PII
C;Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology

Query Match      100.0%; Score 33; DB 2; Length 70;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
   |||::|||
Db 6 FOAGPRVCLG 15

RESULT 8
D81003
hypothetical protein NME2131 [imported] - Neisseria meningitidis (strain MC58 serogroup
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: D81003
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
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ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: D81003
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <TET>
A;Cross-references: UNIPROT:Q9JXB9; UNIPARC:UPI000000C487B; GB:AE002561; GB:AE002098; NID
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NME2131

Query Match      100.0%; Score 33; DB 2; Length 71;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
   |||::|||
Db 2 FKLGVYTCLG 11

RESULT 9
D82025
probable integral membrane protein NMA0300 [imported] - Neisseria meningitidis (strain Z22)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: D82025
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
.; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D82025
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <PAR>
A;Cross-references: UNIPROT:Q9JWM3; UNIPARC:UPI000000C4944; GB:AL162752; GB:AL157959; NID
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA0300

Query Match      100.0%; Score 33; DB 2; Length 71;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXGXXCXG 10
   |||::|||
Db 2 FKLGVYACLG 11

RESULT 10
T17791
hypothetical protein a294R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17791
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17791
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-74 <GRA>
A;Cross-references: UNIPROT:Q84610; UNIPARC:UPI000000P54FP; EMBL:U42580; NID:g4028896; PII
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: a294R

Query Match      100.0%; Score 33; DB 2; Length 74;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FXXGXXXCXG 10
|::|::|::|::|
Db 16 FFKGASTCEG 25

RESULT 11

T01646
apoptotic cell death regulator DAD1 homolog - maize (fragment)
N;Alternate names: apoptosis suppressor; defender against cell death 1 protein
C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 31-Dec-2004
C;Accession: T01646
R;Finkelstein, D.B.; Drew, M.C.; Jordan, W.R.; Wing, R.A.; Mullet, J.E.; Morgan, P.W.
submitted to the EMBL Data Library, March 1998
A;Description: Apoptotic gene discovery in maize.
A;Reference number: Z14356
A;Accession: T01646
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-78 <FIN>
A;Cross-references: UNIPARC:UPI0000178A85; EMBL:AF055909; NID:g3264593; PIDN:AAC24568.1;
A;Experimental source: strain TX5855
C;Genetics:
A;Gene: dad1
C;Superfamily: Defender against cell death DAD
C;Keywords: apoptosis

Query Match 100.0%; Score 33; DB 2; Length 78;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|::|
Db 23 FLSGLVSCIG 32

RESULT 12

S38926
hypothetical protein 14 - phage phi-C31
C;Species: phage phi-C31
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S38926
R;Hartley, N.M.; Murphy, G.O.; Bruton, C.J.; Chater, K.F.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38912
A;Accession: S38926
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <HAR>
A;Cross-references: UNIPROT:Q38035; UNIPARC:UPI000009AEB0; EMBL:X76288; NID:g432610; PID
C;Genetics:
A;Start codon: GTG

Query Match 100.0%; Score 33; DB 2; Length 80;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|::|
Db 16 FPSGPTYCEG 25

RESULT 13

T17723
hypothetical protein a232R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17723
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17723

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-87 <GRA>
A;Cross-references: UNIPROT:Q84552; UNIPARC:UPI00000F617B; EMBL:U42580; NID:g4028896; PID
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: a232R

Query Match 100.0%; Score 33; DB 2; Length 87;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|::|
Db 26 FTGSEKCSG 35

RESULT 14

T06524
probable cytochrome P450 - garden pea (fragment)
N;Contains: oxidoreductase (EC 1.1.1.1)
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06524
R;Frank, M.R.; Deyneka, J.M.; Schuler, M.A.
Plant Physiol. 110, 1035-1046, 1996
A;Title: Cloning of wound-induced cytochrome P450 mono-oxygenases expressed in pea.
A;Reference number: Z15734; MUID:96417083; PMID:8819874
A;Accession: T06524
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-89 <FRA>
A;Cross-references: UNIPROT:Q40985; UNIPARC:UPI000009PA6B; EMBL:U29334; NID:g894154; PIDN
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; monooxygenase; oxidoreductase

Query Match 100.0%; Score 33; DB 2; Length 89;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|::|
Db 25 FRSGRRGCPG 34

RESULT 15

AE2692
hypothetical protein Atu0941 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE2692
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <KUR>
A;Cross-references: UNIPROT:Q8UGU4; UNIPARC:UPI00000D19AD; GB:AE008688; PIDN:AAL41955.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0941
A;Map position: circular chromosome

Query Match 100.0%; Score 33; DB 2; Length 96;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
Db 18 FLIGVLFCG 27

RESULT 16

A75635
cytochrome P450-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
A;Accession: A75635
R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
Science 286, 1571-1577, 1999
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-103 <WHI>
A;Cross-references: UNIPROT:Q9RZ12; UNIPARC:UPI0000003B6F; GB:AE001827; NID:96460959; PT
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRC0001
A;Map position: plasmid
A;Genome: plasmid
A;Note: plasmid CP1
C;Superfamily: Deinococcus radiodurans cytochrome P450-related protein DRC0001

Query Match 100.0%; Score 33; DB 2; Length 103;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
Db 63 FGKGEHACLG 72

RESULT 17

B82914
hypothetical protein UU225.1 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
A;Accession: B82914
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-112 <GLA>
A;Cross-references: UNIPARC:UPI000000C1BDB; GB:AE002123; GB:AF222894; NID:96899229; PIDN:
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU225.1
A;Genetic code: SGC3

Query Match 100.0%; Score 33; DB 2; Length 112;
Best Local Similarity 40.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
Db 76 FVFGILCLG 85

RESULT 18

A54437
apoptotic cell death regulator DAD1 - human
C;Species: Homo sapiens (man)
C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004

C;Accession: A54437

R;Nakashima, T.; Sekiguchi, T.; Kuraoka, A.; Fukushima, K.; Shibata, Y.; Komiyama, S.; Ni
Mol. Cell. Biol. 13, 6367-6374, 1993

A;Title: Molecular cloning of a human cDNA encoding a novel protein, DAD1, whose defect c
A;Reference number: A54437; MUID:94019310; PMID:8413235

A;Accession: A54437

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-113 <NAK>

A;Cross-references: UNIPROT:P61803; UNIPARC:UPI00000040DF; GB:D15057; NID:9493244; PIDN:

A;Experimental source: transformed Raji cells

A;Note: sequence extracted from NCBI backbone (NCBIN:137990, NCBIP:137993)

C;Superfamily: Defender against cell death DAD

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 40.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|

Db 56. FLSGFISCVG 65

RESULT 19

C54437

apoptotic cell death regulator DAD1 - golden hamster

C;Species: Mesocricetus auratus (golden hamster)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 31-Dec-2004

A;Accession: C54437

R;Nakashima, T.; Sekiguchi, T.; Kuraoka, A.; Fukushima, K.; Shibata, Y.; Komiyama, S.; Ni

Mol. Cell. Biol. 13, 6367-6374, 1993

A;Title: Molecular cloning of a human cDNA encoding a novel protein, DAD1, whose defect c

A;Reference number: A54437; MUID:94019310; PMID:8413235

A;Accession: C54437

A;Molecule type: mRNA

A;Residues: 1-113 <NAK>

A;Cross-references: UNIPROT:P61806; UNIPARC:UPI00000040DF; GB:D15058; NID:9493235; PIDN:

A;Experimental source: BHK21 cell line

C;Superfamily: Defender against cell death DAD

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 40.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|

Db 56 FLSGFISCVG 65

RESULT 20

I49285

defender against apoptotic cell death protein 1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004

A;Accession: I49285; S65658

R;Apte, S.S.; Mattei, M.G.; Seldin, M.F.; Olsen, B.R.

FEBS Lett. 363, 304-306, 1995

A;Title: The highly conserved defender against the death 1 (DAD1) gene maps to human chr

A;Reference number: I49285; MUID:95255568; PMID:7737422

A;Accession: I49285

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-113 <RES>

A;Cross-references: UNIPROT:P61804; UNIPARC:UPI0000047517; EMBL:U22107; NID:9849126; PIDN:

A;Molecule type: mRNA

A;Accession: S65658

A;Residues: 1-113 <APT>

A;Cross-references: UNIPARC:UPI0000047517; GB:U22107; NID:9849126; PIDN:AAA85855.1; PIDN:

C;Genetics:

A;Gene: DAD1

A;Map position: 14

C;Superfamily: Defender against cell death DAD

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 40.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 56 FLSGVLSCIG 65

RESULT 21
 T03016
 probable apoptotic cell death regulator DAD1 - rice
 C;Species: Oryza sativa (rice)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
 C;Accession: T03016
 R;Tanaka, Y.; Makishima, T.; Sasabe, M.; Ichinose, Y.; Shiraiishi, T.; Nishimoto, T.; Yam
 Plant Cell Physiol. 38, 383-397, 1997
 A;Title: Dad-1, a putative programmed cell death gene in rice.
 A;Reference number: Z14819
 A;Accession: T03016
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 1-114 <TAN>
 A;Cross-references: UNIPROT:O50070; UNIPARC:UPI0000128DE9; EMBL:D89726; PIDN:BAA24072.1
 A;Experimental source: cultivar Nipponbare
 C;Genetics:
 A;Gene: DAD-1
 C;Superfamily: Defender against cell death DAD

Query Match 100.0%; Score 33; DB 2; Length 114;
 Best Local Similarity 40.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 58 FLSGVLSCIG 67

RESULT 22
 S71269
 apoptotic cell death regulator DAD1 homolog - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
 C;Accession: S71269
 R;Cooke, M.R.
 submitted to the EMBL Data Library, February 1996
 A;Reference number: S71269
 A;Accession: S71269
 A;Molecule type: mRNA
 A;Residues: 1-115 <COO>
 A;Cross-references: UNIPROT:Q39080; UNIPARC:UPI0000128DE1; EMBL:X95585; NID:g1184192; PI
 C;Superfamily: Defender against cell death DAD
 C;Keywords: apoptosis

Query Match 100.0%; Score 33; DB 2; Length 115;
 Best Local Similarity 40.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 59 FLSGVLSCIG 68

RESULT 23
 F86446
 probable defender against cell death protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
 C;Accession: F86446
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: F86446
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-115 <STO>
 A;Cross-references: UNIPROT:Q39080; UNIPARC:UPI0000162F4A; GB:AE005172; NID:g10801366; PI
 C;Genetics:
 A;Map position: 1
 C;Superfamily: Defender against cell death DAD

Query Match 100.0%; Score 33; DB 2; Length 115;
 Best Local Similarity 40.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 59 FLSGVLSCIG 68

RESULT 24
 T17016
 defender against cell death 1 homolog - apple tree
 C;Species: Malus domestica (apple tree)
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
 C;Accession: T17016
 R;Dong, Y.H.; Atkinson, R.G.; Morris, B.A.; Gardner, R.C.
 submitted to the EMBL Data Library, August 1996
 A;Description: An apple mRNA with high homology to the human DAD-1 gene.
 A;Reference number: Z18653
 A;Accession: T17016
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 1-119 <DON>
 A;Cross-references: UNIPROT:O24060; UNIPARC:UPI0000128DE8; EMBL:U68560; NID:g1546826; PI
 A;Experimental source: strain Granny Smith
 C;Genetics:
 A;Gene: DAD-1
 C;Superfamily: Defender against cell death DAD
 C;Keywords: apoptosis

Query Match 100.0%; Score 33; DB 2; Length 119;
 Best Local Similarity 40.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 63 FLSGVLSCIG 72

RESULT 25
 T39694
 hypothetical protein SPAC17A3.02 - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T39694
 R;Wood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, July 1999
 A;Reference number: Z21870
 A;Accession: T39694
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-119 <WOO>
 A;Cross-references: UNIPROT:Q9UUF4; UNIPARC:UPI000006A199; EMBL:AL109652; PIDN:CAB51761.
 A;Experimental source: strain 972h-; cosmid cl7A3
 C;Genetics:
 A;Gene: SPDB:SPAC17A3.02
 A;Map position: 2

A;Introns: 23/1; 28/1; 59/2; 66/1

Query Match 100.0%; Score 33; DB 2; Length 119;
Best Local Similarity 40.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 44 FVPGCLLCGG 53

RESULT 26

H87152
hypothetical protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87152
R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
cam, M.A.; Rutherford, K.W.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: H87152
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <STO>
A;Cross-references: UNIPROT:Q9CHH8; UNIPARC:UPI0000006E17; GB:AL450380; NID:gl3093604; F
C;Genetics:
A;Gene: ML1949

Query Match 100.0%; Score 33; DB 2; Length 119;
Best Local Similarity 40.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 2 FWVGRCGG 11

RESULT 27

T39039
probable oligosaccharyl transferase epsilon subunitdefender against cell death homolog
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T39039
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21797
A;Accession: T39039
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-122 <GEN>
A;Cross-references: UNIPROT:O14238; UNIPARC:UPI00000130EE7; EMBL:Z98981; PIDN:CAB11729.1;
A;Experimental source: strain 972h-; cosmid c6f6
C;Genetics:
A;Gene: SPDB:SPAC6F6.05
A;Map position: 1
A;Introns: 101/2
C;Superfamily: Defender against cell death DAD

Query Match 100.0%; Score 33; DB 2; Length 122;
Best Local Similarity 40.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 58 FLSGFISCVG 67

RESULT 28

T38989

hypothetical protein SPAC630.11 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38989

R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Zimmermann, W.; Wambutt, R.
submitted to the EMBL Data Library, August 1999

A;Reference number: Z21822

A;Accession: T38989

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-122 <MCD>

A;Cross-references: UNIPROT:Q9UHL; UNIPARC:UPI0000069E76; EMBL:AL109832; PIDN:CAB52733.

A;Experimental source: strain 972h-; cosmid c630

C;Genetics:

A;Gene: SPDB:SPAC630.11

A;Map position: 1

A;Introns: 6/2; 12/3; 37/1; 59/2; 78/1

C;Superfamily: Saccharomyces probable membrane protein YJR044C

Query Match 100.0%; Score 33; DB 2; Length 122;
Best Local Similarity 40.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 67 FTFGATCTG 76

RESULT 29

T05467

hypothetical protein T805.60 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05467

R;Bavan, M.; Medler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schueller

submitted to the Protein Sequence Database, February 1998

A;Reference number: Z15417

A;Accession: T05467

A;Molecule type: DNA

A;Residues: 1-124 <BEV>

A;Cross-references: UNIPROT:O49708; UNIPARC:UPI00000A83C8; EMBL:AL021890

A;Experimental source: cultivar Columbia; BAC clone T805

C;Genetics:

A;Map position: 4

A;Introns: 40/2; 92/3

A;Note: T805.60

C;Superfamily: hypothetical protein YCL033C

Query Match 100.0%; Score 33; DB 2; Length 124;
Best Local Similarity 40.0%; Pred. No. 3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|
Db 51 FDDGIYSCAG 60

RESULT 30

I46935

aldehyde dehydrogenase class x - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C;Accession: I46935

R;Algar, E.M.; Cheung, B.; Hayes, J.; Holmes, R.S.; Beacham, I.R.

Adv. Exp. Med. Biol. 328, 153-157, 1993

A;Title: Bovine corneal aldehyde dehydrogenases: evidence for multiple gene products (ALI

A;Reference number: I46935; MUID:93263009; PMID:8493893

A;Accession: I46935

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-126 <ALG>

A;Cross-references: UNIPROT:P52476; UNIPARC:UPI0000129261; GB:SG1045; NID:g300403; PIDN:.

C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 100.0%; Score 33; DB 2; Length 126;
 Best Local Similarity 40.0%; Pred. No. 3e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 24 FSMGQCCCPG 33

RESULT 31
 T28875
 hypothetical protein R04E5.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T28875
 R:Miller, N.
 submitted to the EMBL Data Library, December 1995
 A:Description: The sequence of C. elegans cosmid R04E5.
 A:Reference number: 220535
 A:Accession: T28875
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-132 <MUL>
 A:Cross-references: UNIPARC:UPI0000179CD0; EMBL:U41538; PIDN:AAC48178.1; GSPDB:GNO0028;
 A:Experimental source: strain Bristol N2; clone R04E5
 C:Genetics:
 A:Gene: CESP:R04E5.1
 A:Map position: X
 A:Introns: 31/3; 72/3; 102/1; 125/3

Query Match 100.0%; Score 33; DB 2; Length 132;
 Best Local Similarity 40.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 77 FECGWTCTFG 86

RESULT 32
 S61662
 dolichyl-diphosphooligosaccharide-protein glycotransferase (EC 2.4.1.119) epsilon chain
 N:Alternate names: protein O3211; protein YOR103c; protein YOR3211c
 C:Species: Saccharomyces cerevisiae
 C:Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 31-Dec-2004
 C:Accession: S61662; S62142; S62149; S66988
 R:Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Sander, C.; Valencia
 submitted to the EMBL Data Library, December 1995
 A:Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
 A:Reference number: S61643
 A:Accession: S61662
 A:Molecule type: DNA
 A:Residues: 1-133 <BEN>
 A:Cross-references: UNIPROT:P46964; UNIPARC:UPI0000168417; EMBL:X94335; NID:g1262139; PI
 R:Silberstein, S.; Collins, P.G.; Kelleher, D.J.; Gilmore, R.
 J. Cell Biol. 131, 371-383, 1995
 A:Title: The essential OST2 gene encodes the 16-kD subunit of the yeast oligosaccharyltr
 A:Reference number: S62142; MUID:96017708; PMID:7593165
 A:Accession: S62142
 A:Molecule type: DNA
 A:Residues: 4-133 <SIL>
 A:Cross-references: UNIPARC:UPI0000168A33; EMBL:U32307; NID:g1041719; PIDN:AAC49086.1; E
 A:Accession: S62149
 A:Molecule type: protein
 A:Residues: 5-31,36-43 <SIW>
 A:Cross-references: UNIPARC:UPI0000178A86
 R:Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansoorge, W.
 submitted to the Protein Sequence database, July 1996
 A:Reference number: S66965
 A:Accession: S66988
 A:Molecule type: DNA
 A:Residues: 1-133 <VOS>

A:Cross-references: UNIPARC:UPI0000168417; EMBL:Z75010; NID:g1420282; PIDN:CAA99300.1; P
 A:Experimental source: strain S288C.
 C:Genetics:
 A:Gene: SGD:OST2; OST2
 A:Cross-references: SGD:S0005629
 A:Map position: 15R
 C:Superfamily: Defender against cell death DAD
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
 F:55-71/Domain: transmembrane #status predicted <TM1>
 F:79-95/Domain: transmembrane #status predicted <TM2>
 F:113-129/Domain: transmembrane #status predicted <TM3>

Query Match 100.0%; Score 33; DB 2; Length 133;
 Best Local Similarity 40.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 80 FLAGFIICVG 89

RESULT 33
 F69870
 general stress protein homolog ykzA - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: F69870
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
 Rieger, M.; Rivolta, C.; Rocha, B.; Roche, M.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Seginuchi, J.; Sekowska, A.; Seror,
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: F69870
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-136 <KUN>
 A:Cross-references: UNIPROT:P80242; UNIPARC:UPI00000602B3; GB:Z99110; GB:AL009126; NID:G
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: ykzA
 C:Superfamily: hypothetical protein yk1A

Query Match 100.0%; Score 33; DB 2; Length 136;
 Best Local Similarity 40.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 48 FAAGYAACFG 57

RESULT 34
 S22388
 phospholipase A2 (EC 3.1.1.4) ammodytin I2 precursor - western sand viper
 C:Species: Viper ammodytes ammodytes (western sand viper)
 C:Date: 07-Apr-1994 #sequence_revision 19-May-1994 #text_change 05-Oct-2004
 C:Accession: S22388; S36686; S36685
 R:Krishaj, I.; Liang, N.S.; Fungcar, J.; Strukelj, B.; Ritonja, A.; Gubensek, F.
 Eur. J. Biochem. 204, 1057-1062, 1992
 A:Title: Amino acid and cDNA sequences of a neutral phospholipase A(2) from the long-nos
 A:Reference number: S22388; MUID:92201190; PMID:1551386
 A:Accession: S22388

A;Molecule type: mRNA
A;Residues: 1-137 <KKI>
A;Cross-references: UNIPROT:P34180; UNIPARC:UPI0000131159; EMBL:X56878; NID:G5702035; P1
A;Accession: S36686
A;Status: preliminary
A;Molecule type: protein
A;Residues: 17-137 <XR2>
A;Cross-references: UNIPARC:UPI0000175885
R;Gubensek, F.
submitted to the EMBL Data Library, January 1991
A;Reference number: S36685
A;Accession: S36685
A;Molecule type: mRNA
A;Residues: 1-131, S', 133-137 <GUB>
A;Cross-references: UNIPARC:UPI0000175886; EMBL:X56878; NID:G64450; PIDN:CAA0200.1; PID
C;Superfamily: Phospholipase A2
C;Keywords: calcium; calcium binding; carboxylic ester hydrolase; venom
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-137/Product: amodytin I2 #status predicted <WAT>
F;43,45,47,64/Binding site: calcium (Tyr, Gly, Asp) #status predicted
F;63,105/Active site: His, Asp #status predicted

Query Match 100.0%; Score 33; DB 2; Length 137;
Best Local Similarity 40.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXCXG 10
Db 84 FENGDIVCGG 93
|:|:|:|:|:|

RESULT 35
A95297
hypothetical protein Sma0537 [imported] - Sinorhizobium meliloti (strain 1021) magaplaem
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95297
R;Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: A95297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <KUR>
A;Cross-references: UNIPROT:Q930B7; UNIPARC:UPI000000CB042; GB:AE006469; PIDN:AAK64939.1;
R;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.K.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.P.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Contents: annotation
C;Genetics:
A;Gene: Sma0537
A;Genome: plasmid

Query Match 100.0%; Score 33; DB 2; Length 137;
Best Local Similarity 40.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXCXG 10
Db 85 FATGLDCCG 94
|:|:|:|:|

RESULT 36
G85060
hypothetical protein AT4g04830 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85060
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: G85060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-139 <STO>
A;Cross-references: UNIPROT:Q9ZS91; UNIPARC:UPI00000A7821; GB:NC_001268; NID:G7267241; P1
C;Genetics:
A;Gene: AT4g04830
A;Map position: 4
C;Superfamily: hypothetical protein YCL033C

Query Match 100.0%; Score 33; DB 2; Length 139;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXCXG 10
Db 44 FEEGIFDCVG 53
|:|:|:|:|

RESULT 37
E85060
hypothetical protein AT4g04810 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E85060
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: E85060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-139 <STO>
A;Cross-references: UNIPROT:Q9M025; UNIPARC:UPI00000AB22A; GB:NC_001268; NID:G7267239; P1
C;Genetics:
A;Gene: AT4g04810
A;Map position: 4
C;Superfamily: hypothetical protein YCL033C

Query Match 100.0%; Score 33; DB 2; Length 139;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXCXG 10
Db 44 FEEGIFDCVG 53
|:|:|:|:|

RESULT 38
T05465
hypothetical protein T805.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05465
R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schueller,
submitted to the Protein Sequence Database, February 1998
A;Reference number: Z15417
A;Accession: T05465
A;Molecule type: DNA
A;Residues: 1-141 <BEV>
A;Cross-references: UNIPROT:O49706; UNIPARC:UPI00000AAC95; EMBL:AL021890
A;Experimental source: cultivar Columbia; BAC clone T805
C;Genetics:
A;Map position: 4
A;Introns: 37/2; 89/3
A;Note: T805.40

C;Superfamily: hypothetical protein YCL033c

Query Match 100.0%; Score 33; DB 2; Length 141;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|::|
Db 48 FEGTYSCAG 57

RESULT 39

H85060
hypothetical protein AT4g04840 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85060
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <STO>
A;Cross-references: UNIPROT:Q9M0Z4; UNIPARC:UPI00000A6C24; GB:NC_001268; NID:g7267242; F
C;Genetics:
A;Map position: 4
C;Superfamily: hypothetical protein YCL033c

Query Match 100.0%; Score 33; DB 2; Length 141;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|::|
Db 48 FEGTYSCAG 57

RESULT 40

T26567
hypothetical protein Y26D4A.1 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26567
R;White, S.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20234
A;Accession: T26567
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-141 <WIL>
A;Cross-references: UNIPARC:UPI000017BC51; EMBL:AL110478; NID:e1542139; PIDN:CAB54345.1;
A;Experimental source: clone Y26D4A
C;Genetics:
A;Gene: CESP:Y26D4A.1

Query Match 100.0%; Score 33; DB 2; Length 141;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|::|
Db 123 FHYGVFACEG 132

RESULT 41

T36312
hypothetical protein SCE8.i3c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36312

R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21604
A;Accession: T36312
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-142 <SAU>
A;Cross-references: UNIPROT:Q9Z4W4; UNIPARC:UPI00000DAF25; EMBL:AL035654; PIDN:CAB38591.1
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE8.i3c

Query Match 100.0%; Score 33; DB 2; Length 142;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|::|
Db 75 FNGDSCGCVG 84

RESULT 42

T05466
hypothetical protein T805.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05466
R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schueller
submitted to the Protein Sequence Database, February 1998
A;Reference number: Z15417
A;Accession: T05466
A;Molecule type: DNA
A;Residues: 1-143 <BEV>
A;Cross-references: UNIPROT:O49707; UNIPARC:UPI000009E636; EMBL:AL021890
A;Experimental source: cultivar Columbia; BAC clone T805
C;Genetics:
A;Map position: 4
A;Introns: 39/2; 91/3
A;Note: T805.50
C;Superfamily: hypothetical protein YCL033c

Query Match 100.0%; Score 33; DB 2; Length 143;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|::|::|::|::|
Db 50 FEGTYSCAG 59

RESULT 43

PC4428
cytochrome P450 4C8 - termite (Mastotermes darwiniensis) (fragment)
C;Species: Mastotermes darwiniensis (termite)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: PC4428
R;Faickh, P.H.J.; Balcombe, W.; Haritos, V.S.; Ahokas, J.T.
Biochem. Biophys. Res. Commun. 241, 579-583, 1997
A;Title: Isolation and identification of a cytochrome P450 sequence in an Australian ter
A;Reference number: PC4428; MUID:98086394; PMID:9425314
A;Accession: PC4428
A;Molecule type: mRNA
A;Residues: 1-144 <FAI>
A;Cross-references: UNIPROT:P91762; UNIPARC:UPI00000773EC; GB:U77126; NID:g1684797; PIDN
C;Comment: This protein is involved in oxidation of a wide range of endogenous and exoge
C;Genetics:

A;Gene: CYP4C8
C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein
F;140/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 33; DB 2; Length 144;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|:|:|:|:
Db 133 FSAGPRNCIG 142

RESULT 44
S20227
cytochrome P450 2C4 - rabbit (fragment)
N;Alternate names: cytochrome P450PBC4
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 09-Jul-2004
C;Accession: S20227; S16715
R;Zhao, J.
submitted to the EMBL Data Library, September 1987
A;Reference number: S20227
A;Accession: S20227
A;Molecule type: mRNA
A;Residues: 1-145 <ZHA1>
A;Cross-references: UNIPROT:Q29507; UNIPARC:UPI0000086985; EMBL:M17026; NID:g164932; PID
R;Zhao, J.; Leighton, J.K.; Kemper, B.
Biochem. Biophys. Res. Commun. 146, 224-231, 1987
A;Title: Characterization of rabbit cytochrome P450IIC4 cDNA and induction by phenobarbi
A;Reference number: S16715; MUID:87270743; PMID:3453118
A;Accession: S16715
A;Molecule type: mRNA
A;Residues: 3-145 <ZHA2>
A;Cross-references: UNIPARC:UPI0000174CD4; EMBL:M17026
C;Genetics:
A;Gene: CYP2C4
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo
F;90/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 33; DB 2; Length 145;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|:|:|:|:
Db 83 FSAGKRCVCG 92

RESULT 45
S36442
reverse transcriptase-like protein - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S36442
R;Szemraj, J.; Plucienniczak, G.; Jaworski, J.; Plucienniczak, A.
submitted to the EMBL Data Library, August 1993
A;Description: Evidence for homological recombination with participation of the bovine a
A;Reference number: S36442
A;Accession: S36442
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <S2E>
A;Cross-references: UNIPROT:O97916; UNIPARC:UPI000017C55A; EMBL:Z25525

Query Match 100.0%; Score 33; DB 2; Length 147;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|:|:|:|:
Db 25 FTGKGVCQG 34

RESULT 46
G82223
PilB-related protein VC1236 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82223
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82223
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <HEI>
A;Cross-references: UNIPROT:Q9KSMO; UNIPARC:UPI00000C2F04; GB:AE004203; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1236
A;Map position: 1
C;Superfamily: hypothetical protein YCL033c

Query Match 100.0%; Score 33; DB 2; Length 148;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|:|:|:|:
Db 58 FEPGLYQCAG 67

RESULT 47
S30389
hypothetical protein 2 - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
C;Accession: S30389
R;Berger, W.; Meindl, A.; van de Pol, T.J.R.; Cremers, F.P.M.; Ropers, H.H.; Doerner, C.
E.M.; Meitinger, T.
Nature Genet. 1, 199-203, 1992
A;Title: Isolation of a candidate gene for Norrie disease by positional cloning.
A;Reference number: S30388; MUID:93265103; PMID:1303235
A;Accession: S30389
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-157 <BER>
A;Cross-references: UNIPARC:UPI000011DP5F; EMBL:X65724; NID:g29946; PIDN:CAA46640.1; PID

Query Match 100.0%; Score 33; DB 2; Length 157;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|:|:|:|:|:
Db 114 FPLGSQCCLG 123

RESULT 48
F84769
defender against cell death protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C;Accession: F84769
R;Xin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84769
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 <STO>
A;Cross-references: UNIPARC:UPI0000178A87; GB:AE002093; NID:g3608136; PIDN:AAC36169.1; G
C;Genetics:

A:Gene: At2g35520
A:Map position: 2
C:Superfamily: Defender against cell death DAD

Query Match 100.0%; Score 33; DB 2; Length 160;
Best Local Similarity 40.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXCXG 10
|::|::|:
Db 104 FLGVLSCIG 113

RESULT 49
PC4262
cytochrome P450 monooxygenase (EC 1.-.-.-) BF6-2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: PC4262
R:Maizra, S.; Dombrowski, S.M.; Waters, L.C.; Ganguly, R.
Gene 180, 165-171, 1996
A:Title: Three second chromosome-linked clustered Cyp6 genes show differential constitut
A:Reference number: JC5320; MUID:97128822; PMID:8973362
A:Accession: PC4262
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-162 <MAI>
A:CROSS-references: UNIPROT:Q9V769; UNIPARC:UPI000016BC70; GB:L46858; NID:g1478047; PID:
A:Experimental source: strain 91-R
C:Comment: This enzyme is a microsomal enzyme, and is involved in insecticide resistance
C:Keywords: oxidoreductase

Query Match 100.0%; Score 33; DB 2; Length 162;
Best Local Similarity 40.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXCXG 10
|::|::|:
Db 95 FGDGFRNCIG 104

RESULT 50
155299
Cytochrome P450 PB-1 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I55299
R:Kimura, H.; Sogawa, K.; Sakai, Y.; Fujii-Kuriyama, Y.
J. Biol. Chem. 264, 2338-2342, 1989
A:Title: Alternative splicing mechanism in a cytochrome P-450 (P-450PB-1) gene generated
A:Reference number: I55299; MUID:89123309; PMID:2914909
A:Accession: I55299
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-169 <RES>
A:CROSS-references: UNIPROT:Q64614; UNIPARC:UPI0000056356; GB:M24239; NID:g341144; PIDN:
C:Genetics:
A:Introns: 62/3; 110/1
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; transmembrane protein
F,114/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 33; DB 2; Length 169;
Best Local Similarity 40.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXCXG 10
|::|::|:
Db 107 FSAGKRCAG 116

Search completed: March 8, 2006, 11:24:36
Job time : 41 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 8, 2006, 11:17:59 ; Search time 229 Seconds
(without alignments)
30.809 Million cell updates/sec

Title: US-10-751-235-14

Perfect score: 33

Sequence: 1 FXGXGXXCXG 10

Scoring table: BLOSUM62PX-f

Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot_05_80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	18	2	Q13665_HUMAN
2	33	100.0	21	2	Q9TX62_HELVI
3	33	100.0	30	2	Q6V0Y8_MUSSP
4	33	100.0	32	1	COAT1_BPIF1
5	33	100.0	35	2	Q9P9X1_XYLFA
6	33	100.0	36	2	Q19047_RABIT
7	33	100.0	38	2	Q6LBR9_MOUSE
8	33	100.0	40	2	Q9S918_ARATH
9	33	100.0	44	2	Q9RID5_MOUSE
10	33	100.0	44	2	Q6LBR7_MOUSE
11	33	100.0	45	2	Q14555_HUMAN
12	33	100.0	47	2	Q84NZ2_GOSBA
13	33	100.0	47	2	Q84NZ3_GOSBA
14	33	100.0	47	2	Q84NZ4_GOSBA
15	33	100.0	47	2	Q84NZ5_9ROSI
16	33	100.0	49	2	Q62SA3_BACLD
17	33	100.0	50	1	VG38_BFMD2
18	33	100.0	50	2	Q5K6R0_CRAGI
19	33	100.0	50	2	Q70WU5_9LILI
20	33	100.0	54	2	Q9YH75_9PERC
21	33	100.0	55	2	Q66BR5_YERPS
22	33	100.0	60	2	Q9YH73_SCOMX
23	33	100.0	63	2	Q8GYD1_ARATH
24	33	100.0	64	2	Q58F97_MUSDO
25	33	100.0	64	2	Q81160_HPBVO
26	33	100.0	66	2	Q9Y087_GLORO
27	33	100.0	66	2	Q9F452_9RHIZ
28	33	100.0	66	2	Q915Y3_PSEAE
29	33	100.0	67	2	Q9TX04_CHITE
30	33	100.0	68	2	Q16868_HUMAN
31	33	100.0	68	2	Q75MK4_HUMAN

32	33	100.0	68	2	Q5DN50_9CAUD
33	33	100.0	68	2	Q6GVF0_FRAAN
34	33	100.0	68	2	Q76BJ9_HPBVO
35	33	100.0	68	2	Q7THR3_HPBVO
36	33	100.0	68	2	Q80GT7_HPBVO
37	33	100.0	68	2	Q8AZ65_HPBVO
38	33	100.0	68	2	Q8A4D4_HPBVO
39	33	100.0	68	2	Q931L0_HPBVO
40	33	100.0	68	2	Q9DKQ0_HPBVO
41	33	100.0	68	2	Q4SGY2_TETNG
42	33	100.0	69	2	Q67NC4_SYMTH
43	33	100.0	70	2	Q40986_PEA
44	33	100.0	71	2	Q9JWM3_NEIMA
45	33	100.0	71	2	Q9JXB9_NEIMB
46	33	100.0	71	2	Q8VLR5_9PAPI
47	33	100.0	72	2	Q81WZ9_HUMAN
48	33	100.0	72	2	Q8BC64_9PAPI
49	33	100.0	72	2	Q8JSL4_9PAPI
50	33	100.0	72	2	Q9Q2R1_9PAPI
51	33	100.0	73	2	Q96KF0_HUMAN
52	33	100.0	73	2	Q51D67_PINTA
53	33	100.0	73	2	Q51DC1_PINTA
54	33	100.0	73	2	Q8JSM0_9PAPI
55	33	100.0	74	2	Q58F98_MUSDO
56	33	100.0	74	2	Q4FCQ9_EUSGR
57	33	100.0	74	2	Q84610_CHVP1
58	33	100.0	74	2	Q9YH76_PLAPE
59	33	100.0	75	2	Q5LI59_BACFN
60	33	100.0	76	2	Q9BPX8_RAT
61	33	100.0	77	2	Q4TDK7_TETNG
62	33	100.0	78	2	Q7Y2F7_9CAUD
63	33	100.0	79	1	DAD1_MAIZE
64	33	100.0	79	2	Q570F4_ARATH
65	33	100.0	79	2	Q63ND0_BURPS
66	33	100.0	79	2	Q62AC6_BURMA
67	33	100.0	80	2	Q38035_BPPEC
68	33	100.0	81	2	Q726M1_DESVH
69	33	100.0	82	2	Q54X01_DICDI
70	33	100.0	82	2	Q9TTP6_SHEEP
71	33	100.0	83	2	Q5XNT2_ANOGA
72	33	100.0	84	2	Q72446_HUMAN
73	33	100.0	84	2	P31146_GLYEC
74	33	100.0	85	2	Q6DQ89_MUSAC
75	33	100.0	85	2	Q9IA67_BRARE
76	33	100.0	86	1	GON2_ONCMY
77	33	100.0	86	2	Q5XNS9_ANOGA
78	33	100.0	86	2	Q5XNU4_ANOGA
79	33	100.0	86	2	Q5XNU5_ANOGA
80	33	100.0	86	2	Q94FX5_MAIZE
81	33	100.0	86	2	Q6XAG0_CORCL
82	33	100.0	86	2	Q9PT25_ONCMY
83	33	100.0	87	2	Q84552_CHVP1
84	33	100.0	89	2	Q4L230_PHACH
85	33	100.0	89	2	Q5XNT9_ANOGA
86	33	100.0	89	2	Q40985_PEA
87	33	100.0	89	2	Q4RANI_TETNG
88	33	100.0	90	2	Q54EJ7_DICDI
89	33	100.0	90	2	Q6GV08_MANSE
90	33	100.0	90	2	Q4LDW5_TOBAC
91	33	100.0	91	2	Q5XNU9_ANOGA
92	33	100.0	91	2	Q5XNV0_ANOGA
93	33	100.0	91	2	Q94FX4_MAIZE
94	33	100.0	93	2	Q6TXU6_BRARP
95	33	100.0	94	1	SCYBB_HUMAN
96	33	100.0	94	2	Q12583_CANMA
97	33	100.0	94	2	Q53YAJ_HUMAN
98	33	100.0	94	2	Q8MIZ0_MACMU
99	33	100.0	94	2	Q58D69_BOVIN
100	33	100.0	95	2	Q5XW75_ANOGA

ALIGNMENTS

```
RESULT 1
Q13665 HUMAN
ID Q13665 HUMAN PRELIMINARY; PRT; 18 AA.
AC Q13665;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Cardiac myosin binding protein (fragment).
GN Name=MyBP-C;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96083592; PubMed=7493025;
RA Watkins H., Conner D., Thierfelder L., Jarcho J.A., MacRae C.,
RA McKenna W.J., Maron B.J., Seidman J.G., Seidman C.E.;
RT "Mutations in the cardiac myosin binding protein-C gene on chromosome
RT 11 cause familial hypertrophic cardiomyopathy.";
RL Nat. Genet. 11:434-437(1995).
DR EMBL; S80805; AAB35661.1; -; mRNA.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1891 MW; 3EC942CE85A19C97 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 2 FDGGIYVCGG 11

RESULT 2
Q9TX62 HELVI
ID Q9TX62 HELVI PRELIMINARY; PRT; 21 AA.
AC Q9TX62;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome P-450 (fragment).
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94178422; PubMed=8131898;
RA Hodgson E., Rose R.L., Goh D.K., Rock G.C., Roe R.M.;
RT "Insect cytochrome P-450: metabolism and resistance to insecticides.";
RL Biochem. Soc. Trans. 21:1060-1065(1993).
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome P450.
SQ SEQUENCE 21 AA; 2422 MW; DF21177CB719B5F2 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 8 FCLGPRNCIG 17

RESULT 3
Q6V0Y8 MUSSP
ID Q6V0Y8 MUSSP PRELIMINARY; PRT; 30 AA.
AC Q6V0Y8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
```

```
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome P450 4a10 (Fragment).
GN Name=CYP4a10;
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Liver;
RA Ruiz-Laguna J., Abril N., Pueyo C.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AY355164; AAQ55849.1; -; mRNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome P450.
DR InterPro; IPR002403; EP450IV.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00465; EP450IV.
DR PROSITE; PS00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
FT NON_TER 30
SQ SEQUENCE 30 AA; 3290 MW; D3A0937E3E70515E CRC64;

Query Match 100.0%; Score 33; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 11 FSGGARNCIG 20

RESULT 4
COAT1 BP1F1
ID COAT1 BP1F1 STANDARD; PRT; 32 AA.
AC O80295;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Coat protein C, polypeptide I.
GN Name=VII; Synonyms=7;
OS Bacteriophage If1.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10868;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Hill D.F., Hughes G., McNaughton J.C., Stockwell P.A., Petersen G.B.;
RT "DNA sequence of the filamentous coliphage If1.";
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
CC -I- SUBUNIT: Coat protein C is composed of two subunits, polypeptide I
CC (gene VII) and polypeptide II (gene IX) (by similarity).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U02303; AAC62152.1; -; Genomic DNA.
DR Capsid protein; Structural protein.
KW Capsid protein; Structural protein.
SQ SEQUENCE 32 AA; 3394 MW; E0365E0A002B50AA CRC64;

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 40.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 FXXGXXCXG 10
|:|:|:|:|:
Db 14 FNAGLVICFG 23

RESULT 5

Q9P9X1_XYLPA PRELIMINARY; PRT; 35 AA.
AC Q9P9X1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf2749;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=945c;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.D., Hohnsbeil J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.P., Truffi D., Tsai S.M., Tsuchioka M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "the genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
DR EMBL; AE004081; AAF85534.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 35 AA; 3787 MW; D84CD0D69718029E CRC64;

Query Match 100.0%; Score 33; DB 2; Length 35;
Best Local Similarity 40.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXCXG 10
|:|:|:|:|:
Db 5 FDAGAAICVG 14

RESULT 6

O19047_RABIT
ID O19047_RABIT PRELIMINARY; PRT; 36 AA.
AC O19047;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
DE ORF36.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stengelin S., Becker W., Maier M., Rosenberger J., Kramer W.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ002005; CAA05134.1; -; Genomic DNA.
SQ SEQUENCE 36 AA; 3844 MW; 5B872DD29C85E956 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 36;
Best Local Similarity 40.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXCXG 10
|:|:|:|:|:
Db 2 FRKGLKVCRG 11

RESULT 7

Q6LBR9_MOUSE PRELIMINARY; PRT; 38 AA.
AC Q6LBR9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE D3 class I MHC gene (exon 5) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Domesticus.
RX PubMed=2584927; DOI=10.1084/jem.170.6.1837;
RA Brorson K.A., Hunt S.W. III, Hunkapiller T., Sun Y.H., Cheroutre H.,
RA Nickerson D.A., Hood L.;
RT "Comparison of exon 5 sequences from 35 class I genes of the BALB/c mouse";
RL J. Exp. Med. 170:1837-1858(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Domesticus;
RA Brorson K.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; X16198; CAG82020.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 38 38
SQ SEQUENCE 38 AA; 4176 MW; 25428879345A1085 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 38;
Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXCXG 10
|:|:|:|:|:
Db 7 FQGNHCSCG 16

RESULT 8

Q9S9I8_ARATH PRELIMINARY; PRT; 40 AA.
AC Q9S9I8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Modification methylase (BC 2.1.1.73) (Cytosine-specific methyltransferase) (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

```
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93281384; PubMed=8389441;
RA Finnegan E.J., Dennis E.S.;
RT "Isolation and identification by sequence homology of a putative
RT cytosine methyltransferase from Arabidopsis thaliana.";
RL Nucleic Acids Res. 21:2383-2388(1993).
DR PIR; S35641; S35641.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR001525; C5_DNA_meth.
DR Pfam; PF00145; DNA_methylase; 1.
DR PROSITE; PS00094; C5_MTASE_1; 1.
FT NON TER 1
FT NON TER 16
FT NON TER 17
FT NON TER 40
FT NON TER 40
SQ SEQUENCE 40 AA; 4448 MW; 33A7296755138EA7 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:::|:|
Db 2 FINGPPCQG 11

RESULT 9
Q9R1D5_MOUSE PRELIMINARY; PRT; 44 AA.
ID Q9R1D5_MOUSE PRELIMINARY; PRT; 44 AA.
AC Q9R1D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Phosphodiesterase I/nucleotide pyrophosphatase (Fragment).
GN Name=Enpp2; Synonym=Npps2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvJ;
RX MEDLINE=20169177; PubMed=10702660;
RA Piao J.-H., Mateuda Y., Nakamura H., Sano K.;
RT "Assignment of Enpp2, the gene encoding phosphodiesterase I/nucleotide
RT pyrophosphatase 2, to mouse Chromosome 15D2.";
RL Cytogenet. Cell Genet. 87:172-174(1999).
DR EMBL; AF128879; AAD50640.1; -; Genomic_DNA.
DR MGI; MGI:1321390; Enpp2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
FT NON TER 44
FT NON TER 44
SQ SEQUENCE 44 AA; 4840 MW; 905BB935D7F1BF1F CRC64;

Query Match 100.0%; Score 33; DB 2; Length 44;
Best Local Similarity 40.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:::|:|
Db 18 FAIGNVLCIG 27

RESULT 10
Q6LBR7_MOUSE PRELIMINARY; PRT; 44 AA.
ID Q6LBR7_MOUSE PRELIMINARY; PRT; 44 AA.
AC Q6LBR7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
```

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Q1 class I MHC gene (exon 5) (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Domesticus;
RX PubMed=2584927; DOI=10.1084/jem.170.6.1837;
RA Brorson K.A., Hunt S.W. III, Hunkapiller T., Sun Y.H., Cheroutre H.,
RA Nickerson D.A., Hood L.;
RT "Comparison of exon 5 sequences from 35 class I genes of the BALB/c
RT mouse.";
RL J. Exp. Med. 170:1837-1858(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Domesticus;
RX Brorson K.;
RA Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
RL EMBL; X16200; CAB82022.1; -; Genomic_DNA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphodiesterase I alpha (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96163899; PubMed=8586446;
RA Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J.,
RA Nakamura H., Sano K.;
RT "Molecular cloning and chromosomal assignment of the human brain-type
RT phosphodiesterase I/nucleotide.";
RL Genomics 30:380-384(1995).
DR EMBL; D45914; BAA08342.1; -; Genomic_DNA.
FT NON TER 45
FT NON TER 45
SQ SEQUENCE 45 AA; 5014 MW; 69C831AD365E889D CRC64;

Query Match 100.0%; Score 33; DB 2; Length 45;
Best Local Similarity 40.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXXCXG 10
|:::|:|
Db 18 FAVGNVLCIG 27

RESULT 12
Q84NZ2_GOSBA PRELIMINARY; PRT; 47 AA.
ID Q84NZ2_GOSBA PRELIMINARY; PRT; 47 AA.
AC Q84NZ2;
```



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RX MEDLINE=22569057; PubMed=12679546; DOI=10.1093/molbev/msq065;
RA Sanchina D.S., Alvarez I., Cronn R.C., Liu B., Rong J., Noyes R.D.,
RA Paterson A.H., Wing R.A., Wilkins T.A., Wendel J.F.;
RT "Rate variation among nuclear genes and the age of polyploidy in
RL Gossypium.";
RL Mol. Biol. Evol. 20:633-643(2003).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AF525941; AAP05781.1; -; Genomic_DNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP450I.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
FT NON_TER 1
FT NON_TER 47
FT NON_TER 47
SQ SEQUENCE 47 AA; 5106 MW; 8A53B1DCB6D7C951 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 47;
Best Local Similarity 40.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXXCG 10
Db 13 FGAGRRICAG 22

RESULT 16
Q62SA3_BACLD
ID Q62SA3_BACLD PRELIMINARY; PRT; 49 AA.
AC Q62SA3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BL02399;
OS Bacillus licheniformis (strain DSM 13 / ATCC 14580).
OC Bacillia; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15461803;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,
RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
RA Ehrlich S.D., Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).
DR EMBL; CP000002; AAU24356.1; -; Genomic_DNA.
DR InterPro; IPR010070; Cons hypoth. TTM.
DR TIGRFAMs; TIGR01732; Clny_TM_Bac11; 1.
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 4794 MW; 5FDF1724D0001D5B CRC64;

Query Match 100.0%; Score 33; DB 2; Length 49;
Best Local Similarity 40.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXXCG 10
Db 3 FGYGCGCGG 12

RESULT 17
VG38_BPMD2
ID VG38_BPMD2 STANDARD; PRT; 50 AA.
AC O64229;
DT 15-DEC-1998 (Rel. 37, Created)
```

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DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Gene 38 protein (Gp38).
GN Name=38;
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC L5-like viruses.
OC NCBI_TaxID=28369;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=98300335; PubMed=9636706; DOI=10.1006/jmbi.1997.1610;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: implications for phage
RT evolution.";
RL J. Mol. Biol. 279:143-164(1998).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF022214; AAC18479.1; -; Genomic_DNA.
CC PIR; D72804; D72804.
CC SEQUENCE 50 AA; 4851 MW; 75BCC1A1CF2EP26E CRC64;

Query Match 100.0%; Score 33; DB 1; Length 50;
Best Local Similarity 40.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXXXXXCG 10
Db 13 FALGLTACDG 22

RESULT 18
Q5K6R0_CRAGI
ID Q5K6R0_CRAGI PRELIMINARY; PRT; 50 AA.
AC Q5K6R0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cytochrome P450 related protein (P-fragment).
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoidae; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cardiac;
RA Lopes E., Ohresser M.C.P., Cancela M.L.;
RT "Identification and expected function of some genes differentially
RT expressed in either heart or heart-derived cell cultures in
RT Crassostrea gigas: a new approach to better understanding Bivalvia
RT primary cell culture.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AF075692; AAQ13473.1; -; mRNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP450I.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
FT NON_TER 1
FT NON_TER 50
FT NON_TER 50
SQ SEQUENCE 50 AA; 5802 MW; 191409A96CDC85BA CRC64;

Query Match 100.0%; Score 33; DB 2; Length 50;
Best Local Similarity 40.0%; Pred. No. 5.8e+02;
```

Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXCXG 10
|:|:|:|:|:
Db 31 FVGRRRCVG 40

RESULT 19

Q70WU5_9LILI PRELIMINARY; PRT; 50 AA.
AC Q70WU5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Dad-1 homologue (Fragment).
GN Name=dadi;
OS Alstroemeria hybrid cultivar 'Samora'.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Alstroemeriaceae;
OC Alstroemeria.
OX NCBI_TaxID=160840;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Petal.
RA Wagstaff C., Malcolm P., Rafiq A., Leverenz M., Griffiths G.,
RA Thomas B., Stead A., Rogers H.;
RT "Programmed cell death (PCD) processes begin extremely early in
RT Alstroemeria petal senescence.";
RL New Phytol. 160:49-59(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Petal;
RA Rogers H.J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ514409; CAD5820.1; -; mRNA.
DR InterPro; IPR003038; DAD.
DR Pfam; PF02109; DAD; 1.
FT NON TER 1 1
FT NON TER 50 50
SQ SEQUENCE 50 AA; 5463 MW; 46455530700E0A80 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 50;
Best Local Similarity 40.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXCXG 10
|:|:|:|:|:
Db 8 FLSGLSCVG 17

RESULT 20

Q9YH75_9PERC PRELIMINARY; PRT; 54 AA.
AC Q9YH75;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome P450 1A (Fragment).
GN Name=CYP1A1;
OS Ammodytes tobianus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Perciformes;
OC Trachinoidei; Ammodytidae; Ammodytes.
OX NCBI_TaxID=84621;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Robertson F.E., McPhail M.E., Stagg R.M., Craft J.A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AJ130768; CAA10203.1; -; mRNA.
DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP4501.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
FT NON TER 1 1
FT NON TER 54 54
SQ SEQUENCE 54 AA; 6181 MW; 0429CF02A404D8E8 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 54;
Best Local Similarity 40.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXCXG 10
|:|:|:|:|:
Db 35 FGLGKRCIG 44

RESULT 21

Q66BRS_YERPS PRELIMINARY; PRT; 55 AA.
ID Q66BRS_YERPS PRELIMINARY;
AC Q66BRS;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative phage minor tail protein.
GN OrderedLocustNames=YPTB1705;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype 1;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Rubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH20944.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 55 AA; 6624 MW; D20E1ADD3FF2F29D CRC64;

Query Match 100.0%; Score 33; DB 2; Length 55;
Best Local Similarity 40.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXGXXCXG 10
|:|:|:|:|:
Db 24 FVLGTHCWG 33

RESULT 22

Q9YH73_SCOMX PRELIMINARY; PRT; 60 AA.
ID Q9YH73_SCOMX PRELIMINARY;
AC Q9YH73;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome P450 1A (Fragment).
GN Name=CYP1A1;
OS Scophthalmus maximus (Turbot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciforma; Pleuronectiformes;
OC Pleuronectoidae; Scophthalmidae; Scophthalmus.

```
OX NCBI_TaxID=52904;
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Robertson F.E., McPhail M.E., Stagg R.M., Craft J.A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AJ130770; CAA10205.1; -; mRNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002403; EP450IV.
DR Pfam; PF00067; P450_1.
DR PRINTS; PR00465; EP450IV.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Iron; Metal-binding.
FT NON TER 1 60
FT NON TER 60 60
SQ SEQUENCE 60 AA; 6988 MW; 5379CF03ED02A142 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 60;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 41 FGLGRRRCIG 50

RESULT 23
Q8GXD1_ARATH PRELIMINARY; PRT; 63 AA.
ID Q8GXD1_ARATH PRELIMINARY;
AC Q8GXD1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein At1g57750/T8L23_21.
GN Name=At1g57750/T8L23_21;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju K., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK118299; BAC42917.1; -; mRNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450_1.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 63 AA; 7063 MW; 5D00C1D972039F85 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 63;
Best Local Similarity 40.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 3 FNSGPRTCIG 12

RESULT 24
Q58F97_MUSDO PRELIMINARY; PRT; 64 AA.
ID Q58F97_MUSDO PRELIMINARY;
AC Q58F97;
```

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DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
OC Muscidae; Musca.
OX NCBI_TaxID=7370;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ma C.X., Qiu X.H., Li M., He F.Q., Liu H.X.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AY960134; AAX54885.1; -; mRNA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
FT NON TER 1 1
FT NON TER 64 AA; 7184 MW; 597E70ECAP195DF8 CRC64;
SQ SEQUENCE 64 AA; 7184 MW; 597E70ECAP195DF8 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 64;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 2 FGEGRNCIG 11

RESULT 25
Q81160_HPBVO PRELIMINARY; PRT; 64 AA.
ID Q81160_HPBVO PRELIMINARY;
AC Q81160;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface antigen (HBSAG).
OS Hepatitis B virus.
OC Viruses; Retro-transcribing viruses; Hepadnaviridae;
OC Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85107103; PubMed=3968537;
RA Takeshima H., Inokoshi J., Namiki M., Shimada J., Omura S.;
RT "Structural analysis of the gene coding for hepatitis B virus surface
RT antigen and its product."
RL J. Gen. Virol. 66:195-200(1985).
DR EMBL; M23808; AAA45500.1; -; mRNA.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfac.
DR PANTHER; PTHR10832; Hepvir_surfac; 1.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 64 AA; 6842 MW; 122E2B1D040D755 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 64;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 41 FLGGAPTCLG 50

RESULT 26
Q9Y087_GLORO PRELIMINARY; PRT; 66 AA.
ID Q9Y087_GLORO PRELIMINARY;
AC Q9Y087;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
```


01-NOV-1999 (Tremblrel. 12, Last sequence update)
01-JUN-2003 (Tremblrel. 24, Last annotation update)
Aldehyde dehydrogenase (Fragment).
Name=adh-1;
OS Globodera rostochiensis (Golden nematode worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
OX NCBI_TaxID=31243;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Qiu L., Schots A., Smant G., Bakker J., Helder J.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133109; CAB45527.1; -, mRNA.
DR HSP; P05091; 1002.
DR SMR; Q9Y087; 10-66.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR02086; Aldehyd dehydrog.
DR Pfam; PF00171; Aldehyd; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; 1.
KW Oxidoreductase.
FT NON TER 1 1
FT NON TER 66 66
SQ SEQUENCE 66 AA; 7168 MW; FAFAP2FA8F831A8 CRC64;
Query Match 100.0%; Score 33; DB 2; Length 66;
Best Local Similarity 40.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGXXXXXG 10
|:::|:::|
DB 45 FNOGQCCAG 54
RESULT 27
Q9F452_9RHIZ
ID Q9F452_9RHIZ PRELIMINARY; PRT; 66 AA.
AC Q9F452;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE P-450-type monooxygenase (fragment).
GN Name=virH2;
OS Agrobacterium tumefaciens.
OG Plasmid pTi15955.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=358;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88247765; PubMed=2837739;
RA Thompson D.V., Melchers L.S., Idler K.B., Shilperoort R.A.,
RA Hooikaas P.J.J.;
RT Analysis of the complete nucleotide sequence of the Agrobacterium
RT tumefaciens virB operon.;
RL Nucleic Acids Res. 16:4621-4636 (1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Schrammeijer B., Beijersbergen A., Idler K.B., Melchers L.S.,
RA Thompson D.V., Hooikaas P.J.J.;
RT "Sequence analysis of the vir-region from Agrobacterium tumefaciens
RT octopine Ti plasmid pTi15955.";
RL J. Exp. Bot. 347:1167-1169 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Thompson D.;
RL Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Schrammeijer B.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.

DR EMBL; X06826; CAC15160.1; -, Genomic_DNA.
DR HSP; Q9L142; IGWI.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase; Plasmid.
FT NON TER 1 1
SQ SEQUENCE 66 AA; 7329 MW; 824AC9FE080AADF CRC64;
Query Match 100.0%; Score 33; DB 2; Length 66;
Best Local Similarity 40.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGXXXXXG 10
|:::|:::|
DB 8 FGSPPHCPG 17
RESULT 28
Q9I5Y3_PSEAE
ID Q9I5Y3_PSEAE PRELIMINARY; PRT; 66 AA.
AC Q9I5Y3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PA0553;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huftnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL; AS004492; AAG03942.1; -, Genomic_DNA.
DR PIR; A83575; A83575.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 66 AA; 7030 MW; 67FFE399CDF97712 CRC64;
Query Match 100.0%; Score 33; DB 2; Length 66;
Best Local Similarity 40.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGXXXXXG 10
|:::|:::|
DB 11 FCLGLAACSG 20
RESULT 29
Q9TX04_CHITE
ID Q9TX04_CHITE PRELIMINARY; PRT; 67 AA.
AC Q9TX04;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE CE75=E75A ecdysteroid receptor homolog (fragment).
OS Chironomus tentans (Midge).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7153;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9608569; PubMed=7579577;
RA Wegmann I.S., Quack S., Spindler K.D., Dorsch-Haasler K., Vogtli M.,
RA Lezzi M.;
RT "Immunological studies on the developmental and chromosomal
RT distribution of ecdysteroid receptor protein in Chironomus tentans.";
RL Arch. Insect Biochem. Physiol. 30:95-114(1995).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR HSPSP; P03372; IHCQ.
DR SMR; Q9TX04; 1-67.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004879; F:ligand-dependent nuclear receptor activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR000324; Vttd receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR PRINTS; PR00350; VITAMINDR.
DR SMART; SM00399; Znf C4; 1.
DR PROSITE; PS00031; NUCLEAR_REC_DBD_1; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON_TER 1
FT NON_TER 67
SQ SEQUENCE 67 AA; 7822 MW; 42558F74AD1AE611 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 67;
Best Local Similarity 40.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 11 PHYGVHSCG 20

RESULT 30
Q16868 HUMAN PRELIMINARY; PRT; 68 AA.
AC Q16868;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CYP2E1 protein (Fragment).
GN Name=CYP2E1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95251674; PubMed=7733943;
RA Serce E.M., Botto F., Pisano P., Lechevalier E., Desobry A., Barra Y.;
RA "Evidence for the existence of two human CYP2E1 cDNAs using different
RA polyadenylation signals.";
RL Biochem. Biophys. Res. Commun. 209:717-722(1995).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; S77873; AAD14267.1; -; mRNA.
DR HSPSP; P11712; 10Q2.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP450I.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
FT NON_TER 68
FT NON_TER 68
SQ SEQUENCE 68 AA; 7602 MW; 594C69404F84E0F2 CRC64;

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Query Match 100.0%; Score 33; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 5 FSAGKRVGAG 14

RESULT 31
Q75MK4 HUMAN PRELIMINARY; PRT; 68 AA.
AC Q75MK4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein STK17A (Fragment).
GN Name=STK17A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaanty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du P., Lamar B., Courtney L., Kalicki J.,
RA Ozerky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowski-Reilly A., Leonard S., Rohlif T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baerbach R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Glaser E., Lamar B., LaPlant Y., Stoneking T.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011738; AAS02010.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 68
FT NON_TER 68
SQ SEQUENCE 68 AA; 6886 MW; D298AB1D7BBEC5A8 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
Db 11 PHYGVHSCG 20

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Db 55 PQGYSYLCPG 64

RESULT 32
Q5DN50_9CAUD
ID Q5DN50_9CAUD PRELIMINARY; PRT; 68 AA.
AC Q5DN50_9CAUD
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Gp55.
GN ORENAMES=JL001P55;
OS Bacteriophage phi J1001.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=279383;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lohr J.E., Chen P., Hill R.T.;
RT "Genomic Analysis of Bacteriophage PhiJ1001: Insights into Its
RT Interaction with a Sponge-Associated Alpha-Proteobacterium.";
RL Appl. Environ. Microbiol. 71:1598-1609(2005).
DR EMBL; AY576273; AAT69531.1; -; Genomic DNA.
DR InterPro; IPR001128; Cytochrome_P450.
SQ SEQUENCE 68 AA; 7666 MW; 78D629C164309F70 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXXCG 10
|:::|:::|
Db 26 FGQWFECLG 35

RESULT 33
Q6GVF0_FRAAN
ID Q6GVF0_FRAAN PRELIMINARY; PRT; 68 AA.
AC Q6GVF0_FRAAN
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Fragaria ananassa (Strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=3747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Achene;
RA Balogh A., Koncz T., Kiss E., Heszy L.E.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AY633994; AAT46620.1; -; mRNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EF4501.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EF4501.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
FT NON_TER 1 68
FT NON_TER 68 68
SQ SEQUENCE 68 AA; 7416 MW; 9D32752B90EB217 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXXCG 10
|:::|:::|
Db 6 FGAGRICPG 15

RESULT 34
Q76BJ9_HPBVO
ID Q76BJ9_HPBVO PRELIMINARY; PRT; 68 AA.
AC Q76BJ9_HPBVO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE HBS antigen.
OS Hepatitis B virus.
OC Viruses; Retro-transcribing viruses; Hepadnaviridae;
OC Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tanaka Y., Yeo A.E., Orito E., Ito K., Hirashima N., Ide T., Sata M.,
RA Mizokami M.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB111113; BAD02901.1; -; Genomic DNA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfac.
DR PANTHER; PTHR10832; Hepvir_surfac; 1.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 68 AA; 7163 MW; 7351D6EAA55E17AD CRC64;

Query Match 100.0%; Score 33; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXXCG 10
|:::|:::|
Db 41 FLGGAPACPG 50

RESULT 35
Q7THR3_HPBVO
ID Q7THR3_HPBVO PRELIMINARY; PRT; 68 AA.
AC Q7THR3_HPBVO
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Truncated S protein.
OS Hepatitis B virus.
OC Viruses; Retro-transcribing viruses; Hepadnaviridae;
OC Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MH534978;
RA Zhang J.M., Wen Y.M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY220700; AAP40757.1; -; Genomic DNA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfac.
DR PANTHER; PTHR10832; Hepvir_surfac; 1.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 68 AA; 7220 MW; 668BE6EAA545161D CRC64;

Query Match 100.0%; Score 33; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGXXXXXCG 10
|:::|:::|
Db 41 FLGGAPACPG 50

RESULT 36
Q8GTG7_HPBVO
ID Q8GTG7_HPBVO PRELIMINARY; PRT; 68 AA.
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AC Q80G77;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Truncated S protein.
 OS Hepatitis B virus.
 OC Viruses; Retro-transcribing viruses; Hepadnaviridae;
 OC Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FMU022;
 RA Lin X., Zheng D.L., Xu X.;
 RL Submitted (DDBJ-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY206393; AAP06652.1; -; Genomic DNA.
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surfaG.
 DR PANTHER; PTHR10832; Hepvir_surfaG; 1.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 SQ SEQUENCE 68 AA; 7235 MW; 777BE6EAB994DB1D CRC64;

Query Match 100.0%; Score 33; DB 2; Length 68;
 Best Local Similarity 40.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 41 FLGGTTVCLG 50

RESULT 37

Q8AZ65 HPBV0
 ID Q8AZ65 HPBV0 PRELIMINARY; PRT; 68 AA.
 AC Q8AZ65;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 10-MAR-2005 (TrEMBLrel. 30, Last annotation update)
 DE Clone S6.5, complete genome (Clone S6.7, complete genome).
 OS Hepatitis B virus.
 OC Viruses; Retro-transcribing viruses; Hepadnaviridae;
 OC Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Vaishali C., Acharya S.K., Panda S.K.;
 RA "Cryptic Hepatitis B virus infection: analysis of the complete genomic
 RT sequence of HBV from nine patients with seronegative viral
 RT hepatitis";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY161154; AAO12677.1; -; Genomic DNA.
 DR EMBL; AY161156; AAO12688.1; -; Genomic DNA.
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surfaG.
 DR PANTHER; PTHR10832; Hepvir_surfaG; 1.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 SQ SEQUENCE 68 AA; 7323 MW; 10DF16EF5B6C073F CRC64;

Query Match 100.0%; Score 33; DB 2; Length 68;
 Best Local Similarity 40.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 41 FLGGTTVCLG 50

RESULT 38

Q8B4D4 HPBV0
 ID Q8B4D4 HPBV0 PRELIMINARY; PRT; 68 AA.
 AC Q8B4D4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Clone S6.2, complete genome.
 OS Hepatitis B virus.
 OC Viruses; Retro-transcribing viruses; Hepadnaviridae;
 OC Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Vaishali C., Acharya S.K., Panda S.K.;
 RT "Cryptic Hepatitis B virus infection: analysis of the complete genomic
 RT sequence of HBV from nine patients with seronegative viral
 RT hepatitis";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY161151; AAO12668.1; -; Genomic DNA.
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surfaG.
 DR PANTHER; PTHR10832; Hepvir_surfaG; 1.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 SQ SEQUENCE 68 AA; 7295 MW; D3DF16EF59276A8B CRC64;

Query Match 100.0%; Score 33; DB 2; Length 68;
 Best Local Similarity 40.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
 |::|::|::|
 Db 41 FLGGTTVCLG 50

RESULT 39

Q991L0 HPBV0
 ID Q991L0 HPBV0 PRELIMINARY; PRT; 68 AA.
 AC Q991L0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Truncated envelope protein.
 OS Hepatitis B virus.
 OC Viruses; Retro-transcribing viruses; Hepadnaviridae;
 OC Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B11;
 RA Dong J., Cheng J., Wang Q.H., Shi S.S., Hong Y., Huangfu J.K.,
 RA Wang G., Li L., Si C.W.;
 RT "The study on quasispecies of hepatitis b virus: reverse transcriptase
 RT region in polymerase gene as an example";
 RL Ping Tu Hsueh Pao 17:270-272 (2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B11;
 RA Dong J., Cheng J., Huangfu J.K., Hong Y., Wang G., Chen C.G., Li L.,
 RA Zhang L.X., Chen J.M.;
 RT "The preliminary study on individually characterized quasispecies of
 RT hepatitis B virus";
 RL Jie Fang Jun Yi Xue Za Zhi 27:119-121 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B11;
 RA Dong J., Cheng J., Wang Q.H., Shi S.S., Hong Y., Huangfu J.K.,
 RA Wang G., Li L., Si C.W.;
 RT "The study on quasispecies of hepatitis B virus: reverse transcriptase
 RT region in polymerase gene as an example";
 RL Jie Fang Jun Yi Xue Za Zhi 26:823-825 (2002).
 DR EMBL; AF335734; AAK19537.1; -; Genomic DNA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surfaG.
 DR PANTHER; PTHR10832; Hepvir_surfaG; 1.
 DR Pfam; PF00695; VMSA; 1.

KW Antigen; Envelope protein.
SQ SEQUENCE 68 AA; 7182 MW; A59A071AB6A159D CRC64;
Query Match 100.0%; Score 33; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXKGGXXKXG 10
|::|::|::|::|
Db 41 FLGGASTCPG 50

RESULT 40
Q9DKQ0_HPBV0
ID Q9DKQ0_HPBV0 PRELIMINARY; PRT; 68 AA.
AC Q9DKQ0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mutant envelope protein.
OS Hepatitis B virus.
OC Viruses; Retro-transcribing viruses; Hepadnaviridae;
OC Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dong J., Cheng J., Wang Q.H., Shi S.S., Hong Y., Huangfu J.K.,
RA Wang G., Li L., Si C.W.;
RA "The study on quasiespecies of hepatitis B virus: reverse transcriptase
RT region in polymerase gene as an example.";
RL Ping Tu Hsueh Pao 17:270-272(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Dong J., Cheng J., Huangfu J.K., Hong Y., Wang G., Chen C.G., Li L.,
RA Zhang L.X., Chen J.M.;
RA "The preliminary study on individually characterized quasiespecies of
RT hepatitis B virus.";
RL Jie Fang Jun Yi Xue Za Zhi 27:119-121(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Dong J., Cheng J., Wang Q.H., Shi S.S., Hong Y., Huangfu J.K.,
RA Wang G., Li L., Si C.W.;
RA "The study on quasiespecies of hepatitis B virus: reverse transcriptase
RT region in polymerase gene as an example.";
RL Jie Fang Jun Yi Xue Za Zhi 26:823-825(2002).
DR EMBL; AF329859; AAG48739.1; -; Genomic_DNA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surflg; 1.
DR PANTHER; PTHR10832; Hepvir_surflg; 1.
DR Pfam; PF00695; VMSA; 1.
KW Antigen; Envelope protein.
SQ SEQUENCE 68 AA; 7220 MW; 669A071AAB752B1D CRC64;
Query Match 100.0%; Score 33; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXKGGXXKXG 10
|::|::|::|::|
Db 41 FLGGASTCPG 50

RESULT 41
Q4SGY2_TETNG
ID Q4SGY2_TETNG PRELIMINARY; PRT; 68 AA.
AC Q4SGY2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 14 SCAF14590, whole genome shotgun sequence.
GN ORFNames=GSTENG00018412001;
OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Actinomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Nicaud S., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014590; CAG00100.1; -; Genomic_DNA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR PRINTS; PR00463; EP4501.
KW Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 68 AA; 7920 MW; E367B1591080F9B6 CRC64;
Query Match 100.0%; Score 33; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXKGGXXKXG 10
|::|::|::|::|
Db 30 FALGPRSLG 39

RESULT 42
Q67NC4_SYMTH
ID Q67NC4_SYMTH PRELIMINARY; PRT; 69 AA.
AC Q67NC4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=STH1834;
OS Syntrophobacterium thermophilum.
OC Bacteria; Actinobacteria; Syntrophobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IAM14863;
RX PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsui T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of Syntrophobacterium thermophilum, an uncultivable
RT bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944(2004).
DR EMBL; AF006840; BAD40819.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 69 AA; 7618 MW; 50F6B384E1DF1C3F CRC64;
Query Match 100.0%; Score 33; DB 2; Length 69;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 49 FALGDASC 58

RESULT 43
Q0986_PEA PRELIMINARY; PRT; 70 AA.
AC Q0986;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pisum sativum clone MFRTPCR62 wound-inducible cytochrome P450
DE (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Wounded;
RX MEDLINE=96417083; PubMed=8819874; DOI=10.1104/pp.110.3.1035;
RA Frank M.R., Deyneka J.M., Schuler M.A.;
RT "Cloning of wound-induced cytochrome P450 monooxygenases expressed in
pea";
RL Plant Physiol. 110:1035-1046(1996).
DR EMBL; U29335; A49190.1; -; mRNA.
DR PIR; T06525; T06525
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
FT INCON TER 1
SQ SEQUENCE 70 AA; 7952 MW; F8E8E7CA1752CA23 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 70;
Best Local Similarity 40.0%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 6 FQAGPRVCLG 15

RESULT 44
Q9JWM3_NEIMA PRELIMINARY; PRT; 71 AA.
AC Q9JWM3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative integral membrane protein.
GN OrderedLocusNames=NM0300;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491";
RL Nature 404:502-506(2000).
DR EMBL; AL162752; CAB83605.1; -; Genomic_DNA.
DR PIR; D82025; D82025.
KW Complete proteome.

SQ SEQUENCE 71 AA; 8104 MW; 50BE1A62D021F67E CRC64;

Query Match 100.0%; Score 33; DB 2; Length 71;
Best Local Similarity 40.0%; Pred. No. 8.1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 2 FRLGVYACLG 11

RESULT 45
Q9JXB9_NEIMB PRELIMINARY; PRT; 71 AA.
AC Q9JXB9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=NMB2131;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Masiagnani V., Pizzi M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58";
RL Science 287:1809-1815(2000).
DR EMBL; AE002098; AAF42439.1; -; Genomic_DNA.
DR PIR; D81003; D81003.
DR TIGR; NMB2131; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 71 AA; 8091 MW; 4A25DBB87621F66B CRC64;

Query Match 100.0%; Score 33; DB 2; Length 71;
Best Local Similarity 40.0%; Pred. No. 8.1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGXGXXCXG 10
|::|::|::|
Db 2 FRLGVYACLG 11

RESULT 46
Q8VIR5_9PAPI PRELIMINARY; PRT; 71 AA.
AC Q8VIR5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major capsid protein (fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22676373; PubMed=12791874;
DOI=10.1128/JCM.41.6.2509-2514.2003;
RA Antonsson A., Karanfilovska S., Lindqvist P.G., Hansson B.G.;
RT "General acquisition of human papillomavirus infections of skin occurs

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in early infancy."
J. Clin. Microbiol. 41:2509-2514 (2003).
EMBL; AF455145; AAL57872.1; -; Genomic_DNA.
HSSP; Q9WPH4; 1DZL.
GO; GO:0019028; C:Viral capsid; IEA.
GO; GO:0005198; F:Structural molecule activity; IEA.
InterPro; IPR002210; PV_capsid_L1.
Pfam; PF00500; Late_protein_L1; 1.
PRINTS; PR00865; HPV_Capsid_L1.
ProDom; PD000544; PV_capsid_L1; 1.
FT NON TER 1 71
FT NON TER 71 71
SQ SEQUENCE 71 AA; 7998 MW; 8F7DDC13BB31393B CRC64;

Query Match 100.0%; Score 33; DB 2; Length 71;
Best Local Similarity 40.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
Db 33 FIVGCTPCIG 42

RESULT 47
Q8IWZ9_HUMAN
ID Q8IWZ9_HUMAN PRELIMINARY; PRT; 72 AA.
AC Q8IWZ9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 25, Last annotation update)
DE Hypertension associated protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Choi I., Moon K.D., Song I., Wiley J.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF519545; AAN7120.1; -; Genomic_DNA.
DR SRR; Q8IWZ9; 1-71
DR Ensembl; ENSG00000111664; Homo sapiens.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR ProDom; PD000018; WD40; 1.
DR SMART; SM00320; WD40; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW WD repeat.
FT NON TER 1 71
FT NON TER 72 72
SQ SEQUENCE 72 AA; 7993 MW; B61C9DEF13DBEC64 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 72;
Best Local Similarity 40.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
Db 2 FPNGEAICTG 11

RESULT 48
Q8BC64_9PAPI
ID Q8BC64_9PAPI PRELIMINARY; PRT; 72 AA.
AC Q8BC64;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major capsid protein (Fragment).
OS Human papillomavirus.

Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Antonsson A., Eifurt C., Hazard K., Holmgren V., Simon M., Kataoka A.,
Hossain S., Hakangard C., Hansson B.G.;
RT "Prevalence and type spectrum of human papillomaviruses in healthy
skin samples collected in three continents.";
J. Gen. Virol. 84:1881-1886 (2003).
DR EMBL; AF542100; AAN28675.1; -; Genomic_DNA.
DR HSSP; Q9WPH4; 1DZL.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
InterPro; IPR002210; PV_capsid_L1.
Pfam; PF00500; Late_protein_L1; 1.
PRINTS; PR00865; HPV_Capsid_L1.
ProDom; PD000544; PV_capsid_L1; 1.
FT NON TER 1 72
FT NON TER 72 72
SQ SEQUENCE 72 AA; 8182 MW; 6765F1107AC17C82 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 72;
Best Local Similarity 40.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
Db 33 FIVGCTPCIG 42

RESULT 49
Q8JSL4_9PAPI
ID Q8JSL4_9PAPI PRELIMINARY; PRT; 72 AA.
AC Q8JSL4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major capsid protein (Fragment).
OS Chimpanzee papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae; primate papillomaviruses.
NCBI_TaxID=203380;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Antonsson A., Hansson B.G.;
RT "Healthy skin of many animal species harbors papillomaviruses which
are closely related to their human counterparts.";
J. Virol. 76:12537-12542 (2002).
DR EMBL; AF488687; AAM97872.1; -; Genomic_DNA.
DR HSSP; Q9WPH4; 1DZL.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
InterPro; IPR002210; PV_capsid_L1.
Pfam; PF00500; Late_protein_L1; 1.
PRINTS; PR00865; HPV_Capsid_L1.
ProDom; PD000544; PV_capsid_L1; 1.
FT NON TER 1 72
FT NON TER 72 72
SQ SEQUENCE 72 AA; 7953 MW; CEBAA6474A7F27D0 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 72;
Best Local Similarity 40.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXGXXXCXG 10
|::|::|::|
Db 33 FIVGCTPCIG 42
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RESULT 50
Q9Q2RI_9PAPI PRELIMINARY; PRT; 72 AA.
AC Q9Q2RI;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major capsid protein L1 (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20541962; PubMed=11090162;
RX DOI=10.1128/JVI.74.24.11636-11641.2000;
RA Antonsson A., Forslund O., Ekberg H., Sterner G., Hansson B.G.;
RT "The ubiquity and impressive genomic diversity of human skin
RL J. Virol. 74:11636-11641(2000).
RL EMBL; AF217681; AAF25471.1; -; Genomic_DNA.
DR HSSP; Q9WPH4; 1DZL.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; Late_protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
DR PRODOM; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT NON_TER 72
SQ SEQUENCE 72 AA; 8060 MW; 695D736F8F2CBA4B CRC64;
Query Match 100.0%; Score 33; DB 2; Length 72;
Best Local Similarity 40.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FXGXGXXCXG 10
Db 33 FIVGCTPCIG 42
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Search completed: March 8, 2006, 11:23:55
Job time : 236 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: March 7, 2006, 21:43:16 ; Search time 118.8 Seconds
(without alignments)
142.531 Million cell updates/sec

Title: US-10-751-235-10

Perfect score: 122

Sequence: 1 LVAEVSFELFGSGFAIAGPLWTA 24

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122	100.0	539	2	Q6TBX7 ARATH
2	122	100.0	552	2	Q8RWV4 ARATH
3	118	96.7	566	2	Q9SCF8 ARATH
4	110	90.2	584	2	Q9AV27 ORYSA
5	57	46.7	344	1	SVFA BACSK
6	56	45.9	324	2	Q9CF7 LACLA
7	56	45.9	344	1	SVFA BACHD
8	55.5	45.5	470	2	Q5FFI9 GLUOX
9	55	45.1	339	1	SVFA GEOSL
10	55	45.1	350	2	Q8YJ78 ANASP
11	54	44.3	593	2	Q9C6S0 ARATH
12	54	44.3	595	2	Q93VK5 ARATH
13	52.5	43.0	97	2	Q8NQS2 CORGL
14	52	42.6	321	1	LPXK RICCN
15	52	42.6	321	1	LPXK RICRI
16	52	42.6	321	2	Q7P9K9 RICSI
17	52	42.6	325	1	LPXK RICMO
18	52	42.6	325	2	Q4UN11 RICPE
19	52	42.6	344	1	SVFA GEOKA
20	51.5	42.2	68	2	Q6MJ94 BDEBA
21	51.5	42.2	296	2	Q4TSR2 9SPHN
22	51	41.8	339	1	SVFA THETN
23	51	41.8	375	2	Q7M860 WOLSU
24	51	41.8	1258	2	Q9HED9 NEUCR
25	51	41.8	1709	2	Q93H59 STRAW
26	50	41.0	297	2	Q6HCC7 BACHC
27	50	41.0	297	2	Q632T7 BACCZ
28	50	41.0	350	1	SVFA LIJIN
29	50	41.0	350	1	SVFA LISMF
30	50	41.0	350	1	SVFA LISMO
31	50	41.0	601	2	Q4P0G2 USTWMA

32	50	41.0	670	2	Q5W270 9ENTR	Q5W270 serratia sp
33	50	41.0	718	2	Q7WAV9 BORPA	Q7WAV9 bordetella
34	50	41.0	718	2	Q7WK16 BORBR	Q7WK16 bordetella
35	49.5	40.6	287	2	Q9KCQ8 BACHD	Q9KCQ8 bacillus ha
36	49.5	40.6	524	2	Q89PM1 BRAJA	Q89PM1 bradyrhizob
37	49	40.2	216	2	Q5TWN3 ANOGA	Q5TWN3 anopheles g
38	49	40.2	275	2	Q5SJ53 THET8	Q5SJ53 thermus the
39	49	40.2	275	2	Q72JHS THET2	Q72JHS thermus the
40	49	40.2	287	2	Q9KD24 BACHD	Q9KD24 bacillus ha
41	49	40.2	444	2	Q28493 ARCFU	Q28493 archaeoglob
42	49	40.2	494	1	SYK SULSO	P95970 sulfolobus
43	49	40.2	532	2	Q6C2L7 YARLI	Q6C2L7 yarrowia li
44	49	40.2	572	1	INDY1 DROME	Q9VVT2 drosophila
45	49	40.2	582	2	Q7QIT2 ANOGA	Q7QIT2 anopheles g

ALIGNMENTS

RESULT 1
Q6TBX7 ARATH
ID Q6TBX7 ARATH PRELIMINARY; PRT; 539 AA.
AC Q6TBX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chloroplast carotenoid epsilon-ring hydroxylase.
GN Name=LUT1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:14709673; DOI=10.1073/pnas.2237237100;
RA Tian L., Musetti V., Kim J., Magallanes-Lundback M., DellaPenna D.;
RT "The Arabidopsis LUT1 locus encodes a member of the cytochrome P450
RT family that is required for carotenoid epsilon-ring hydroxylation
RT activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:402-407(2004).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AY424805; AAR83120.1; -, mRNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP4501.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
KW Transmembrane.
SQ SEQUENCE 539 AA; 60555 MW; 4C25C728B676ABEB CRC64;
Query Match 100.0%; Score 122; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVAEVSFELFGSGFAIAGPLWTA 24
|||
Db 144 LVAEVSFELFGSGFAIAGPLWTA 167
RESULT 2
Q8RWV4 ARATH
ID Q8RWV4 ARATH PRELIMINARY; PRT; 552 AA.
AC Q8RWV4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative cytochrome P450 (Fragment).

GN Name=At3g531130;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Iehida J., Jones T.,
 RA Kaniya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; AY091083; AAMI3903.1; -; mRNA.
 DR HSSP; P14779; 1JPZ.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002401; EP4501.
 DR Pfam; PF00067; P450.1.
 DR PRINTS; PR00463; EP4501.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKOWN 1.
 KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
 KW Transmembrane.
 FT NON_TER
 SQ SEQUENCE 552 AA; 62073 MW; C23CF8498B58440 CRC64;
 Query Match 100.0%; Score 122; DB 2; Length 552;
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVAEVEFLFGSGFAIAGPLWTA 24
 Db 157 LVAEVEFLFGSGFAIAGPLWTA 180
 RESULT 3
 Q9SCP8 ARATH PRELIMINARY; PRT; 566 AA.
 AC Q9SCP8;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Cytochrom P450-like protein.
 GN Name=T4D2.60;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
 RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
 RA Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; AL129958; CAB64216.1; -; Genomic_DNA.
 DR PIR; T46159; T46159.
 DR HSSP; P14779; 1JPZ.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002401; EP4501.
 DR Pfam; PF00067; P450.1.
 DR PRINTS; PR00463; EP4501.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKOWN 1.
 KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
 KW Transmembrane.
 SQ SEQUENCE 566 AA; 63596 MW; B884E8996B1A4C7D CRC64;
 Query Match 96.7%; Score 118; DB 2; Length 566;
 Best Local Similarity 100.0%; Pred. No. 4.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVAEVEFLFGSGFAIAGPLWT 23
 Db 144 LVAEVEFLFGSGFAIAGPLWT 166
 RESULT 4
 Q9AV27 ORYSA PRELIMINARY; PRT; 584 AA.
 AC Q9AV27; Q7XCI2;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
 DE Putative cytochrome P450 monooxygenase.
 GN ORFNames=OSJNB0001014.16;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,
 RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
 RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
 RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 RT chromosome 10.";
 RL Science 300:1566-1569(2003).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; AE017117; AAP54891.1; -; Genomic_DNA.
 DR EMBL; AC025783; AAK20054.1; -; Genomic_DNA.
 DR HSSP; P14779; 1JPZ.
 DR Gramene; Q9AV27; -.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002401; EP4501.
 DR Pfam; PF00067; P450.1.
 DR PRINTS; PR00463; EP4501.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKOWN 1.
 KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
 KW Transmembrane.
 SQ SEQUENCE 584 AA; 64798 MW; 1A55160A532DCE83 CRC64;

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Query Match      90.2%; Score 110; DB 2; Length 584;
Best Local Similarity 95.7%; Pred. No. 8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LVAEVSFLFGSGFAIAEGPLWT 23
        |||||
DB      152 LVAEVSFLFGSGFAIAEGALWT 174

RESULT 5
ID _SYFA_BACSK STANDARD; PRT; 344 AA.
AC Q5WEJ5;
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Phenylalanine-tRNA synthetase alpha chain (EC 6.1.1.20)
DE (Phenylalanine--tRNA ligase alpha chain) (PHERS).
GN Name=phes; OrderedLocusNames=ABC2680;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16."
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
CC diphosphate + L-phenylalanyl-tRNA(Phe).
CC -1- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
CC family. Phe-tRNA synthetase alpha chain type 1 subfamily.
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removed.
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EMBL; AP006627; BAD65215.1; -; Genomic_DNA.
DR HAMBL; MF_00281; -; 1.
DR InterPro; IPR004188; Phe tRNA_synth_N.
DR InterPro; IPR004529; PheS.
DR InterPro; IPR002319; tRNA_synth_2d.
DR PANTHER; PTHR11538; tRNA_synth_2d; 1.
DR Pfam; PF02912; Phe tRNA_synth_N; 1.
DR Pfam; PF01409; tRNA_synth_2d; 1.
DR TIGRFAMs; TIGR00468; pheS; 1.
DR PROSITE; PS00862; AA tRNA_LIGASE II; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Magnesium; Metal-binding; Nucleotide-binding; Protein biosynthesis.
FT METAL 256
SQ SEQUENCE 344 AA; 38634 MW; 15F6E8B3556E1CC CRC64;

Query Match      46.7%; Score 57; DB 1; Length 344;
Best Local Similarity 50.0%; Pred. No. 5;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      1 LVAEVSFLFGSGFAIAEGP 20
        :|:|:|:|:|:|:|:|:|
DB      113 VTEIEIFLGLGFSIGEGP 132

RESULT 6
Q9CFC7_LACUA
ID Q9CFC7_LACLA PRELIMINARY; PRT; 324 AA.
AC Q9CFC7;

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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Oxidoreductase.
GN Name=yjP; OrderedLocusNames=L11554;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr-1697R;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malmme K.,
RA Weissbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis esp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
DR ENBL; AB006386; AAK05652.1; -; Genomic_DNA.
DR PIR; B86819; B86819.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000683; GFO/IDH/MOCA_N.
DR InterPro; IPR004104; GFO_IDH/MOCA_C.
DR Pfam; PF01408; GFO_IDH/MOCA_1.
DR Pfam; PF02894; GFO_IDH/MOCA_C; 1.
KW Complete proteome.
SQ SEQUENCE 324 AA; 36603 MW; DBF47D6684EB259C CRC64;

Query Match      45.9%; Score 56; DB 2; Length 324;
Best Local Similarity 50.0%; Pred. No. 6.8;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      5 VSBFLFGSGFAIAEGPLWTA 24
        :|:|:|:|:|:|:|:|:|
DB      182 VLQFLGTGTFDAKGIWSS 201

RESULT 7
SYFA_BACHD STANDARD; PRT; 344 AA.
AC Q9K895;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
DE (Phenylalanine--tRNA ligase alpha chain) (PHERS).
GN Name=phes; OrderedLocusNames=BH3111;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji P., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
CC diphosphate + L-phenylalanyl-tRNA(Phe).
CC -1- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
CC family. Phe-tRNA synthetase alpha chain type 1 subfamily.
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CC -----
CC EMBL; BA00004; BAB06830.1; -; Genomic_DNA.
CC PIR; G84038; G84038.
CC HSP; P27001; 1JJC.
CC HAMAP; MF_00281; -; 1.
CC InterPro; IPR004188; Phe tRNA_synth_N.
CC InterPro; IPR004529; PheS.
CC InterPro; IPR002319; tRNA_synth_2d.
CC InterPro; IPR006195; tRNA_ligase_II.
CC PANTHER; PTHR11538; tRNA-synt_2d; 1.
CC Pfam; PF02912; Phe tRNA-synt_N; 1.
CC Pfam; PF01409; tRNA-synt_2d; 1.
CC TIGRFAMs; TIGR00468; pheS; 1.
CC PROSITE; PS50862; AA tRNA_LIGASE_II; 1.
CC Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Magnesium; Metal-binding; Nucleotide-binding; Protein biosynthesis.
FT METAL 256 256 Magnesium (By similarity).
FT SEQUENCE 344 AA; 38931 MW; 498A039538E7A94C CRC64;

Query Match 45.9%; Score 56; DB 1; Length 344;
Best Local Similarity 47.4%; Pred. No. 7.2;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy 2 VAESFELFGSGFAIAGP 20

Db 114 ITEVEDLFIGLFGSVAEGP 132

RESULT 8

ID Q5FP19 GLUOX PRELIMINARY; PRT; 470 AA.
AC Q5FP19;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Galactose-proton symporter.
GN OrderedLocNames=GOX1971;
OS Gluconobacter oxydans (Gluconobacter suboxydans).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconobacter.
OX NCBI_TaxID=442;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=621H;
RX PubMed=15665824; DOI=10.1038/nbt1062;
RA Prust C., Hoffmeister M., Liesegang H., Wieser A., Fricke W.F.,
RA Ehrenreich A., Gottschalk G., Deppenmeier U.;
RT "Complete genome sequence of the acetic acid bacterium Gluconobacter
oxydans";
RL Nat. Biotechnol. 23:195-200(2005).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC EMBL; CP000009; AA061707.1; -; Genomic DNA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC DR GO; GO:0005351; F:sugar porter activity; IEA.
CC DR GO; GO:0005215; F:transporter activity; IEA.
CC DR GO; GO:0008643; P:carbohydrate transport; IEA.
CC DR InterPro; IPR007114; MFS.
CC DR InterPro; IPR005828; Sub-transporter.
CC DR InterPro; IPR005829; Sug-transporter.
CC DR InterPro; IPR003663; Sugar transp.
CC Pfam; PF00083; Sugar tr; 1.
CC PRINTS; PR00171; SUGTRNSPORT.
CC DR TIGRFAMs; TIGR00879; SP; 1.
CC PROSITE; PS50850; MFS; 1.
CC PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
CC DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 470 AA; 49835 MW; ECBAC911C986E16C CRC64;

Query Match 45.5%; Score 55.5; DB 2; Length 470;

Best Local Similarity 75.0%; Pred. No. 11;
Matches 12; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Oy 9 LFGSGFAIAGGPI-WT 23
Db 365 LFVAGFAIGEGPLVWT 380

RESULT 9

ID SYFA_GEOSL STANDARD; PRT; 339 AA.
AC Q74D00;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
GN (Phenylalanyl-tRNA synthetase alpha chain) (PHERS).
DB Names=PheS; OrderedLocNames=GSU1519;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Ward N.L., Beaman M.J., Dodson R.J.,
RA Madupu R., Brinkac J.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Winn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
environments";
RL Science 302:11967-1969(2003).
CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA (Phe) +
CC diphosphate + L-phenylalanyl-tRNA (Phe).
CC -1- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
CC family. Phe-tRNA synthetase alpha chain type 1 subfamily.

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CC EMBL; AE017180; AAR34893.1; -; Genomic_DNA.
CC HSP; P27001; 1B7Y.
CC TIGR; GSU1519; -.
CC HAMAP; MF_00281; -; 1.
CC InterPro; IPR004188; Phe tRNA_synth_N.
CC InterPro; IPR004529; PheS.
CC InterPro; IPR002319; tRNA-synt_2d.
CC InterPro; IPR006195; tRNA_ligase_II.
CC PANTHER; PTHR11538; tRNA-synt_2d; 1.
CC Pfam; PF02912; Phe tRNA-synt_N; 1.
CC Pfam; PF01409; tRNA-synt_2d; 1.
CC TIGRFAMs; TIGR00468; pheS; 1.
CC PROSITE; PS50862; AA tRNA_LIGASE_II; 1.
CC Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Magnesium; Metal-binding; Nucleotide-binding; Protein biosynthesis.
FT METAL 253 253 Magnesium (By similarity).
FT SEQUENCE 339 AA; 37888 MW; 3A36C6EDC3BC5F6A CRC64;

Query Match 45.1%; Score 55; DB 1; Length 339;
Best Local Similarity 45.0%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OS
OC

CC (By similarity)
CC -1- CATALYTIC ACTIVITY: ATP + (2-N,3-O-bis(3-hydroxytetradecanoyl)-
CC beta-D-glucosaminyl)-(1->6)-(2-N,3-O-bis(3-hydroxytetradecanoyl)-
CC beta-D-glucosaminyl phosphate) = ADP + (2-N,3-O-bis(3-
CC hydroxytetradecanoyl)-4-O-phosphono-beta-D-glucosaminyl)-(1->6)-
CC (2-N,3-O-bis(3-hydroxytetradecanoyl)-beta-D-glucosaminyl
CC phosphate)
CC -1- PATHWAY: Lipid A biosynthesis; sixth step.
CC -1- SIMILARITY: Belongs to the lpxK family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AJ293329; CAC3716.1; -; Genomic DNA.
CC DR HAMAP; MF 00409; -; 1.
CC DR InterPro; IPR003758; LpxK.
CC DR Pfam; PF02606; LpxK; 1.
CC DR TIGRFAMS; TIGR00682; lpxK; 1.
CC KW ATP-binding; Kinase; Lipid A biosynthesis; Lipid synthesis;
CC Nucleotide-binding; Transferase.
CC FT NP BIND 54 61 ATP (Potential).
CC SQ SEQUENCE 321 AA; 36083 MW; 45B6CEB6CC50C0AE CRC64;
Query Match 42.6%; Score 52; DB 1; Length 321;
Best Local Similarity 52.4%; Pred. No. 27;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 LVAEVSEFLGSGFAIAEGPL 21
Db :::::
155 IVSDVSRQRFNGFLIPAGPL 175

Search completed: March 7, 2006, 21:58:09
Job time : 122.8 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 21:43:03 ; Search time 234.8 Seconds
(without alignments)
44.911 Million cell updates/sec

Title: US-10-751-235-10

Perfect score: 122

Sequence: 1 LVAEVEFLFGSGFAIAGPLWTA 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	24	9	AEB16912
2	122	100.0	539	9	AEB16908
3	122	100.0	560	8	ADT56240
4	114	93.4	208	9	AEB16923
5	110	90.2	362	9	AEB16920
6	110	90.2	382	8	ADY22850
7	110	90.2	545	9	AEB16919
8	110	90.2	561	9	AEB16918
9	110	90.2	588	9	AEB16954
10	59	48.4	167	6	ABU25025
11	59	48.4	342	6	ABU25075
12	58	47.5	632	9	AEB16936
13	58	47.5	662	8	ADX67984
14	57	46.7	342	9	AEB16939
15	57	46.7	508	9	AEB16937
16	56	45.9	324	5	ABBS4899
17	56	45.9	344	8	ADS28360
18	54	44.3	579	9	AEB16940
19	54	44.3	595	9	AEB16935
20	52.5	43.0	97	4	AAG91239
21	50	41.0	350	5	ABBA49267
22	50	41.0	350	6	ABU33039
23	49.5	40.6	287	8	ADS28192
24	49	40.2	360	8	ADN25200

25	49	40.2	572	4	ABB60315
26	49	40.2	572	4	ABB66903
27	49	40.2	572	5	ABB79611
28	49	40.2	572	6	ABR40099
29	49	40.2	572	8	ADP64789
30	48	39.3	173	6	ABU20163
31	48	39.3	303	8	ADS21348
32	48	39.3	316	9	ABM91222
33	48	39.3	394	8	ADT76358
34	48	39.3	483	8	ADT87787
35	48	39.3	523	7	ADC61143
36	48	39.3	1032	8	ADJ49445
37	48	39.3	1124	8	ADN20724
38	47.5	38.9	103	3	AAU29352
39	47	38.5	168	4	AAU29352
40	47	38.5	255	8	ADX88517
41	47	38.5	326	8	ADX42528
42	47	38.5	359	8	ADS22754
43	47	38.5	489	8	ADX80107
44	47	38.5	512	8	ABM84611
45	47	38.5	683	7	ABO79928

ALIGNMENTS

RESULT 1					
AEB16912					
ID	AEB16912 standard; peptide; 24 AA.				
XX	AC AEB16912;				
XX	XX				
DT	08-SRP-2005 (first entry)				
XX	XX				
DE	Cytochrome P450 monooxygenase transmembrane domain peptide SEQ ID NO: 10.				
XX	XX				
KW	Pigment; metabolic engineering; antioxidant; transgenic plant;				
KW	cytochrome P450.				
XX	XX				
OS	Unidentified.				
XX	XX				
PN	US2005150002-A1.				
XX	XX				
PD	07-JUL-2005.				
XX	XX				
PF	02-JAN-2004; 2004US-00751235.				
XX	XX				
PR	02-JAN-2004; 2004US-00751235.				
XX	XX				
PA	(DELL/) DELLAPENNA D.				
PA	(TIAN/) TIAN L.				
XX	(KIM/) KIM J.				
PI	Dellapenna D, Tian L, Kim J;				
XX	XX				
DR	WPI; 2005-487984/49.				
XX	XX				
PT	New expression vector comprising a nucleic acid sequence encoding a				
PT	polypeptide having monooxygenase P450 activity, useful in altering the				
PT	carotenoid production in a plant for enhancing production of specific				
XX	carotenoid compounds.				
PS	Claim 6; SEQ ID NO 10; 135pp; English.				
XX	XX				
CC	The present invention relates to genes, proteins and methods comprising				
CC	carotenoid monooxygenases in the cytochrome P450 family. The invention				
CC	also relates to altering carotenoid ratios in plants and microorganisms				
CC	using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The				
CC	invention is useful in altering the carotenoid production in a plant for				
CC	enhancing production of specific carotenoid compounds that are potent				
CC	antioxidants. The present sequence is a cytochrome P450 monooxygenase				
CC	conserved transmembrane domain peptide.				
XX	XX				

CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
 CC and for yield improvement by providing improved plant growth and
 CC development under at least one stress condition. The polynucleotide may
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen
 CC flow, increasing plant tolerance to cold or heat, improving plant
 CC tolerance to extreme osmotic and drought conditions, and improving plant
 CC tolerance to plant pests or pathogens. They can also be used in physical
 CC arrays of molecules, plant breeding markers, computer-based storage and
 CC analysis systems. The present sequence is one of the 5544 plant protein
 CC sequences of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX
 SQ Sequence 560 AA;
 Query Match 100.0%; Score 122; DB 8; Length 560;
 Best Local Similarity 100.0%; Pred. No. 5.6e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAEGPLMTA 24
 |||||
 Db 165 LVAEVSEFLFGSGFAIAEGPLMTA 188

RESULT 4
 AEB16923
 ID AEB16923 standard; protein; 208 AA.
 XX
 AC AEB16923;
 DT 08-SEP-2005 (first entry)
 XX
 DE Sunflower cytochrome P450 97C (CYP97C) protein, SEQ ID NO: 21.
 XX
 KW Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C;
 KW cytochrome P450 97C.
 XX
 OS Helianthus annuus.
 XX
 PN US2005150002-A1.
 XX
 PD 07-JUL-2005.
 XX
 PF 02-JAN-2004; 2004US-00751235.
 XX
 PR 02-JAN-2004; 2004US-00751235.
 XX
 PA (DELL/) DELLAPENNA D.
 PA (TIAN/) TIAN L.
 PA (KIMJ/) KIM J.
 XX
 PI Dellapenna D, Tian L, Kim J;
 XX
 XX WPI; 2005-487984/49.
 DR N-PSDB; AEB16929.
 DR GENBANK; BQ971938.
 XX
 XX New expression vector comprising a nucleic acid sequence encoding a
 PT polypeptide having monooxygenase P450 activity, useful in altering the
 PT carotenoid production in a plant for enhancing production of specific

PT carotenoid compounds.
 XX
 PS Claim 9; SEQ ID NO 21; 135pp; English.
 XX
 CC The present invention relates to genes, proteins and methods comprising
 CC carotenoid monooxygenases in the cytochrome P450 family. The invention
 CC also relates to altering carotenoid ratios in plants and microorganisms
 CC using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The
 CC invention is useful in altering the carotenoid production in a plant for
 CC enhancing production of specific carotenoid compounds that are potent
 CC antioxidants. The present sequence is sunflower cytochrome P450
 CC monooxygenase (CYP97C) protein.
 XX
 SQ Sequence 208 AA;

Query Match 93.4%; Score 114; DB 9; Length 208;
 Best Local Similarity 95.8%; Pred. No. 3.6e-10;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAEGPLMTA 24
 |||||
 Db 29 LVAEVSEFLFGSGFAIAEGSLMTA 52

RESULT 5
 AEB16920
 ID AEB16920 standard; protein; 362 AA.

XX
 AC AEB16920;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE Wheat cytochrome P450 97C (CYP97C) protein, SEQ ID NO: 18.
 XX
 KW Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C;
 KW cytochrome P450 97C.

XX
 OS Triticum aestivum.
 XX
 PN US2005150002-A1.
 XX
 PD 07-JUL-2005.
 XX
 PF 02-JAN-2004; 2004US-00751235.
 XX
 PR 02-JAN-2004; 2004US-00751235.
 XX
 PA (DELL/) DELLAPENNA D.
 PA (TIAN/) TIAN L.
 PA (KIMJ/) KIM J.
 XX
 PI Dellapenna D, Tian L, Kim J;
 XX
 XX WPI; 2005-487984/49.
 DR N-PSDB; AEB16926.
 DR GENBANK; CA497665, BG906289, CA742365, CA742792.

XX
 XX New expression vector comprising a nucleic acid sequence encoding a
 PT polypeptide having monooxygenase P450 activity, useful in altering the
 PT carotenoid production in a plant for enhancing production of specific
 PT carotenoid compounds.

XX
 PS Claim 9; SEQ ID NO 18; 135pp; English.

XX
 CC The present invention relates to genes, proteins and methods comprising
 CC carotenoid monooxygenases in the cytochrome P450 family. The invention
 CC also relates to altering carotenoid ratios in plants and microorganisms
 CC using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The
 CC invention is useful in altering the carotenoid production in a plant for
 CC enhancing production of specific carotenoid compounds that are potent
 CC antioxidants. The present sequence is wheat cytochrome P450 monooxygenase
 CC (CYP97C) protein.

Query Match 90.2%; Score 110; DB 9; Length 545;
 Best Local Similarity 95.7%; Pred. No. 5.1e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAEGPLWT 23
 |||||
 Db 136 LVAEVSEFLFGSGFAIAEGALWT 158
 |||||

RESULT 8
 AEB16918
 ID AEB16918 standard; protein; 561 AA.
 XX
 AC AEB16918;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE Rice cytochrome P450 97C2 (CYP97C2) protein, SEQ ID NO: 16.
 XX
 KW Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C2;
 cytochrome P450 97C2.
 XX
 OS Oryza sativa; japonica cultivar-group.
 XX
 PN US2005150002-A1.
 XX
 PD 07-JUL-2005.
 XX
 PF 02-JAN-2004; 2004US-00751235.
 XX
 PR 02-JAN-2004; 2004US-00751235.
 XX
 PA (DELL/) DELLAPENNA D.
 (TIAN/) TIAN L.
 (KIMJ/) KIM J.
 XX
 PI Dellapenna D, Tian L, Kim J;
 XX
 DR WPI; 2005-487984/49.
 DR EMBL; E017117.
 XX
 PT New expression vector comprising a nucleic acid sequence encoding a
 polypeptide having monooxygenase P450 activity, useful in altering the
 carotenoid production in a plant for enhancing production of specific
 carotenoid compounds.
 XX
 PS Claim 9; SEQ ID NO 16; 135pp; English.
 XX
 CC The present invention relates to genes, proteins and methods comprising
 carotenoid monooxygenases in the cytochrome P450 family. The invention
 also relates to altering carotenoid ratios in plants and microorganisms
 using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The
 invention is useful in altering the carotenoid production in a plant for
 enhancing production of specific carotenoid compounds that are potent
 antioxidants. The present sequence is rice cytochrome P450 monooxygenase
 (CYP97C1) protein.

Query Match 90.2%; Score 110; DB 9; Length 561;
 Best Local Similarity 95.7%; Pred. No. 5.3e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAEGPLWT 23
 |||||
 Db 152 LVAEVSEFLFGSGFAIAEGALWT 174
 |||||

RESULT 9
 AEB16954
 ID AEB16954 standard; protein; 588 AA.
 XX

AC AEB16954;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE Rice cytochrome P450 97B4 (CYP97B4) protein, SEQ ID NO: 52.
 XX
 KW Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97B4;
 cytochrome P450 97B.
 XX
 OS Oryza sativa; japonica cultivar-group.
 XX
 PN US2005150002-A1.
 XX
 PD 07-JUL-2005.
 XX
 PF 02-JAN-2004; 2004US-00751235.
 XX
 PR 02-JAN-2004; 2004US-00751235.
 XX
 PA (DELL/) DELLAPENNA D.
 (TIAN/) TIAN L.
 (KIMJ/) KIM J.
 XX
 PI Dellapenna D, Tian L, Kim J;
 XX
 DR WPI; 2005-487984/49.
 DR EMBL; E017117.
 XX
 PT New expression vector comprising a nucleic acid sequence encoding a
 polypeptide having monooxygenase P450 activity, useful in altering the
 carotenoid production in a plant for enhancing production of specific
 carotenoid compounds.
 XX
 PS Claim 9; SEQ ID NO 52; 135pp; English.
 XX
 CC The present invention relates to genes, proteins and methods comprising
 carotenoid monooxygenases in the cytochrome P450 family. The invention
 also relates to altering carotenoid ratios in plants and microorganisms
 using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The
 invention is useful in altering the carotenoid production in a plant for
 enhancing production of specific carotenoid compounds that are potent
 antioxidants. The present sequence is rice cytochrome P450 monooxygenase
 (CYP97B4) protein.

Query Match 90.2%; Score 110; DB 9; Length 588;
 Best Local Similarity 95.7%; Pred. No. 5.6e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAEGPLWT 23
 |||||
 Db 154 LVAEVSEFLFGSGFAIAEGALWT 176
 |||||

RESULT 10
 ABU25025
 ID ABU25025 standard; protein; 167 AA.
 XX
 AC ABU25025;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #10552.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Clostridium difficile.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX

Query Match 46.7%; Score 57; DB 9; Length 508;
Best Local Similarity 40.9%; Pred. No. 2.4;
Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 LVAEVSRLFGSGFAIAGPLW 22
DB 66 ILAEILEFVNGTGLIPADGEVW 87

Search completed: March 7, 2006, 21:53:06
Job time : 240.8 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	52.5	43.0	94	2	US-09-605-703B-1572	Sequence 1572, Ap
2	49	40.2	194	2	US-09-270-767-59102	Sequence 59102, A
3	49	40.2	230	2	US-09-270-767-43713	Sequence 43713, A
4	48	39.5	316	2	US-09-902-540-10421	Sequence 10421, A
5	47	38.3	683	2	US-09-252-991A-28674	Sequence 28674, A
6	46.5	38.1	190	2	US-09-134-000C-6230	Sequence 6230, Ap
7	46	37.7	55	2	US-09-513-999C-4532	Sequence 4532, Ap
8	46	37.7	80	2	US-09-621-976-5244	Sequence 5244, Ap
9	46	37.7	150	2	US-09-270-767-60566	Sequence 60566, A
10	46	37.7	250	2	US-09-489-039A-10680	Sequence 10680, A
11	45	36.9	102	2	US-09-882-434A-1	Sequence 1, Appli
12	45	36.9	110	2	US-09-376-330-24	Sequence 24, Appl
13	45	36.9	131	2	US-09-513-999C-8015	Sequence 8015, Ap
14	45	36.9	166	2	US-09-621-976-4638	Sequence 4638, Ap
15	45	36.9	185	2	US-09-529-157-6	Sequence 6, Appli
16	45	36.9	185	2	US-09-529-157-7	Sequence 7, Appli
17	45	36.9	204	2	US-09-949-016-9489	Sequence 9489, Ap
18	45	36.9	205	2	US-09-673-395A-205	Sequence 205, App
19	45	36.9	218	2	US-09-543-681A-4284	Sequence 4284, Ap
20	45	36.9	329	2	US-10-152-886-51	Sequence 51, Appl
21	45	36.9	522	1	US-08-305-505-2	Sequence 2, Appli
22	45	36.9	561	2	US-09-489-039A-10642	Sequence 10642, A
23	45	36.9	862	2	US-09-902-540-11888	Sequence 11888, A
24	44	36.1	194	2	US-09-252-991A-31239	Sequence 31239, A
25	44	36.1	519	2	US-09-248-796A-19188	Sequence 19188, A
26	44	36.1	865	1	US-07-803-633A-13	Sequence 13, Appl
27	43	35.2	82	2	US-09-253-991A-23597	Sequence 23597, A

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; ORGANISM: Drosophila melanogaster
US-09-270-767-59102

Query Match      40.2%; Score 49; DB 2; Length 194;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 FLFGGFAIAG 19
Db 128 FLGGGFALAEG 139

RESULT 3
US-09-270-767-43713
; Sequence 43713, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43713
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43713

Query Match      40.2%; Score 49; DB 2; Length 230;
Best Local Similarity 75.0%; Pred. No. 4.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 FLFGGFAIAG 19
Db 164 FLGGGFALAEG 175

RESULT 4
US-09-902-540-10421
; Sequence 10421, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902.540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10421
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10421

Query Match      39.3%; Score 48; DB 2; Length 316;
Best Local Similarity 45.5%; Pred. No. 9.8;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 LVAEVSEFLFGGFAIAGPLM 22
Db 261 LVQGVESGFWQAFALNPPLW 282

RESULT 5
US-09-252-991A-28674
; Sequence 28674, Application US/09252991A
```

```
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28674
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28674

Query Match      38.5%; Score 47; DB 2; Length 683;
Best Local Similarity 56.2%; Pred. No. 36;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LFGSGFAIAGPLWTA 24
Db 440 LFGSFYSVAEGLEMLA 455

RESULT 6
US-09-134-000C-6230
; Sequence 6230, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6230
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6230

Query Match      38.1%; Score 46.5; DB 2; Length 190;
Best Local Similarity 50.0%; Pred. No. 9.4;
Matches 12; Conservative 2; Mismatches 5; Indels 5; Gaps 1;

Qy 1 LVAEVSEFLFG-----SGFAIAG 19
Db 91 LVFSISELLFGLAQAKSGFVIRG 114

RESULT 7
US-09-513-999C-4532
; Sequence 4532, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; Patent No. 6783961
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
```

```
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4532
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -23...-1
; OTHER INFORMATION: score 9.4
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 9
; OTHER INFORMATION: Xaa= * or Lys or Leu or Met
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 11
; OTHER INFORMATION: Xaa= * or Glu or Gly
US-09-513-999C-4532

Query Match      37.7%; Score 46; DB 2; Length 55;
Best Local Similarity 50.0%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 10 FGSGFAIAEGPLWT 23
Db 18 FGSGFCICDGTWT 31

RESULT 8
US-09-621-976-5244
; Sequence 5244, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENST.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5244
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -23...-1
US-09-621-976-5244

Query Match      37.7%; Score 46; DB 2; Length 80;
Best Local Similarity 50.0%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 10 FGSGFAIAEGPLWT 23
Db 18 FGSGFCICDGTWT 31

RESULT 9
US-09-270-767-60566
; Sequence 60566, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517

; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60566
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60566

Query Match      37.7%; Score 46; DB 2; Length 150;
Best Local Similarity 52.6%; Pred. No. 8.6;
Matches 10; Conservative 3; Mismatches 6; Indels 6; Gaps 0;

QY 6 SEPLFGSGFAIAEGPLWTA 24
Db 36 SKFVSAQRFAISEGPLCCA 54

RESULT 10
US-09-489-039A-10680
; Sequence 10680, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10680
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10680

Query Match      37.7%; Score 46; DB 2; Length 250;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 12 SGFAIAEGPLW 22
Db 93 SGFRWAEGPVM 103

RESULT 11
US-09-882-434A-1
; Sequence 1, Application US/09882434A
; Patent No. 6909032
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882,434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 102
; TYPE: PRT
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; ORGANISM: Macadamia integrifolia
US-09-882-434A-1

Query Match      36.9%; Score 45; DB 2; Length 102;
Best Local Similarity 45.0%; Pred. No. 7.9;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LVAEVSEFLFGSGFAIAEGPLW 20
Db 16 LIAMASEVWNGSAFTVWSGP 35

RESULT 12
US-09-376-330-24
; Sequence 24, Application US/09376330
; Patent No. 6399321
; GENERAL INFORMATION:
; APPLICANT: Tessier, Daniel C.
; APPLICANT: Dignard, Daniel
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; TITLE OF INVENTION: Method for screening for
; TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
; TITLE OF INVENTION: and nucleic acid encoding for UGGT
; FILE REFERENCE: 2139-9"US"
; CURRENT APPLICATION NUMBER: US/09/376,330
; CURRENT FILING DATE: 1999-08-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: GALT-S. typ
US-09-376-330-24

Query Match      36.9%; Score 45; DB 2; Length 110;
Best Local Similarity 53.3%; Pred. No. 8.6;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 10 FGSGFAIAEGPLWTA 24
Db 62 FNAGFILXIPLWTA 76

RESULT 13
US-09-513-999C-8015
; Sequence 8015, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8015
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-8015

Query Match      36.9%; Score 45; DB 2; Length 131;
Best Local Similarity 36.4%; Pred. No. 11;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
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```
Qy 1 LVAEVSEFLFGSGFAIAEGPLW 22
Db 24 LSAKSSALFFGNFIVSAIPW 45

RESULT 14
US-09-621-976-4638
; Sequence 4638, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4638
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4638

Query Match      36.9%; Score 45; DB 2; Length 166;
Best Local Similarity 36.4%; Pred. No. 14;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 LVAEVSEFLFGSGFAIAEGPLW 22
Db 24 LSAKSSALFFGNFIVSAIPW 45

RESULT 15
US-09-529-157-6
; Sequence 6, Application US/09529157
; Patent No. 6500939
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi
; APPLICANT: Sekine, Shingo
; TITLE OF INVENTION: cDNAs Coding For Human Proteins Having Transmembrane
; TITLE OF INVENTION: Domains
; FILE REFERENCE: GIN-6711CPUS
; CURRENT APPLICATION NUMBER: US/09/529,157
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCT/JP98/04447
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: JP 9-276270
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-157-6

Query Match      36.9%; Score 45; DB 2; Length 185;
Best Local Similarity 36.4%; Pred. No. 16;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 LVAEVSEFLFGSGFAIAEGPLW 22
Db 24 LSAKSSALFFGNFIVSAIPW 45

Search completed: March 7, 2006, 22:00:14
Job time : 27.8 secs
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; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-5132

Query Match 39.8%; Score 48.5; DB 7; Length 613;
Best Local Similarity 33.3%; Pred. No. 7.3;
Matches 10; Conservative 6; Mismatches 5; Indels 9; Gaps 1;

Qy 2 VAESVFLFGSGFAIA-----EGPLW 22
Db 582 ISGASDFRFGSGFNMGTVDPQKNDGPNW 611

RESULT 3
US-11-087-099-10545
; Sequence 10545, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10545
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(654)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-10545

Query Match 39.8%; Score 48.5; DB 7; Length 654;
Best Local Similarity 33.3%; Pred. No. 7.8;
Matches 10; Conservative 6; Mismatches 5; Indels 9; Gaps 1;

Qy 2 VAESVFLFGSGFAIA-----EGPLW 22
Db 623 ISGASDFRFGSGFNMGTVDPQKNDGPNW 652

RESULT 4
US-10-993-143-19
; Sequence 19, Application US/10993143
; Publication No. US20060036374A1
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology
; APPLICANT: Debe, Derek A.
; APPLICANT: Goddard III, William A.
; TITLE OF INVENTION: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM
; TITLE OF INVENTION: PRIMARY PROTEIN SEQUENCE
; FILE REFERENCE: 54318.8001.US02
; CURRENT APPLICATION NUMBER: US/10/993,143
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: 60/218,016
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 09/905,176
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 19
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Rhodospseudomonas viridis
US-10-993-143-19

Query Match 37.7%; Score 45; DB 6; Length 246;
Best Local Similarity 56.2%; Pred. No. 6.8;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 8 FLFGSGFAIAEGPLWT 23
||| : ||| |||

Db 229 FLTGAFGTIASGPFWT 244

RESULT 5
US-11-098-686-10717
; Sequence 10717, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10717
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10717

Query Match 37.7%; Score 46; DB 7; Length 346;
Best Local Similarity 50.0%; Pred. No. 9.7;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LVAESVFLFGSGFAIAEGP 20
||| : ||| ||| :
Db 207 LVSIQGLGIGFAVANVP 226

RESULT 6
US-10-858-730-112
; Sequence 112, Application US/10858730
; Publication No. US2005025586A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor
US-10-858-730-112

Query Match 36.1%; Score 44; DB 6; Length 295;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 11 GSGFAIAEGPLWTA 24
||| : ||| : |||

RESULT 12

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US-11-186-731-2
; Sequence 2, Application US/11186731
; Publication No. US2005025521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047PIRCPI(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR FILING DATE: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-731-2

Query Match      35.2%; Score 43; DB 7; Length 2630;
Best Local Similarity 39.1%; Pred. No. 2.3e+02;
Matches 9; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy  2 VAEVSEFLFG--SGFAIAEGPLW 22
Db  1850 VAGYGTFAFGDAGGMLGGPMM 1872

RESULT 13
US-11-186-731-5
; Sequence 5, Application US/11186731
; Publication No. US2005025521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047PIRCPI(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR FILING DATE: 2002-02-15
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-731-5

Query Match      35.2%; Score 43; DB 7; Length 7968;
Best Local Similarity 39.1%; Pred. No. 7.4e-02;
Matches 9; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy  2 VAEVSEFLFG--SGFAIAEGPLW 22
Db  7188 VAGYGTFAFGDAGGMLGGPMM 7210

RESULT 14
US-11-087-099-11993
; Sequence 11993, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
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; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11993
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Cytophaga hutchinsonii
US-11-087-099-11993

Query Match      34.8%; Score 42.5; DB 7; Length 461;
Best Local Similarity 56.2%; Pred. No. 45;
Matches 9; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy  11 GSGFAIA--EGPLWT 23
Db  179 GSGYIALKTDGLWT 194

RESULT 15
US-11-072-512-2690
; Sequence 2690, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, KYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2690
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2690

Query Match      34.4%; Score 42; DB 7; Length 444;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy  9 LFGSGFAIAEGPLW 22
Db  55 LLGKGLAALDGPKW 68

Search completed: March 7, 2006, 22:06:38
Job time : 10.4 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 21:53:39 ; Search time 19.2 Seconds
(without alignments)
120.271 Million cell updates/sec

Title: US-10-751-235-10
Perfect score: 122
Sequence: 1 LVAEVSEFLFGSGFAIAGPLWTA 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	96.7	566	2 T46159	cytochrome P450-11
2	56	45.9	324	2 B86819	oxidoreductase ypf
3	56	45.9	344	2 G84038	phenylalanine-tRNA
4	55	45.1	350	2 AP2572	hypothetical prote
5	54	44.3	593	2 F86441	probable cytochrom
6	52	42.6	321	2 D97836	tetraacyldisacchar
7	50	41.0	350	2 AE1227	phenylalanine-tRNA s
8	50	41.0	350	2 AG1580	phenylalanine-tRNA s
9	49.5	40.6	287	2 G83838	oxidoreductase (sh
10	49	40.2	287	2 C83824	ABC transporter (p
11	49	40.2	444	2 D69472	modulation protein
12	49	40.2	494	2 S75398	lysine-tRNA ligase
13	48	39.3	465	2 AC2843	multidrug efflux p
14	48	39.3	465	2 D97620	hypothetical prote
15	48	39.3	493	2 F96596	protein Fln21.12
16	47	38.5	168	2 B85752	thiol peroxidase
17	47	38.5	168	2 JC5504	thioredoxin peroxi
18	47	38.5	168	2 G90866	thiol peroxidase
19	47	38.5	344	1 YFBSA	phenylalanine-tRNA
20	47	38.5	354	2 AB2608	phenylalanine-tRNA
21	47	38.5	360	2 A97330	phenylalanine-tRNA
22	47	38.5	363	2 C87336	serine proteinase
23	47	38.5	429	2 B83257	folypolyglutamate
24	46	37.7	274	2 A25102	reaction center pr
25	46	37.7	337	2 AH0972	lipopolysaccharide
26	46	37.7	341	2 S33464	hypothetical prote
27	46	37.7	342	2 A96581	hypothetical prote
28	46	37.7	351	1 VVVP2B	coat protein VP2 -
29	46	37.7	351	1 VVVPAS	coat protein VP2 -

succinate-semialde
protein C05D11.1
translocan-associ
conserved hypotet
hypothetical prote
oxidoreductase hom
oxidoreductase hom
coat protein VP2 -
phenylalanine-tRNA
hypothetical prote
probable lipopolys
hypothetical prote
hydroxymethylgluta
probable glutamate
probable glutamate
hypothetical prote

ALIGNMENTS

RESULT 1

T46159
Cytochrome P450-like protein - Arabidopsis thaliana
N;Alternate names: protein T4D2.60

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46159

R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, December 1999

A;Reference number: Z23025

A;Accession: T46159

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-566 <NA>

A;Cross-references: UNIPROT:Q9SCP8; UNIPARC:UPI000009D7F9; EMBL:AL132958

A;Experimental source: cultivar Columbia; BAC clone T4D2

C;Genetics:

A;Map position: 3

A;Introns: 183/2; 292/3; 358/3; 392/3; 439/3; 475/3; 503/2; 557/3

A;Note: T4D2.60

C;Superfamily: pea cytochrome P450 CYP97; cytochrome P450 homology

C;Keywords: heme; iron; metalloprotein

F;371-536/Domain: cytochrome P450 homology <P45>

F;514/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 96.7% Score 118; DB 2; Length 566;

Best Local Similarity 100.0%; Pred. No. 1.3e-10; Mismatches 0; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVAEVSEFLFGSGFAIAGPLWT 23

|||||

DB 144 LVAEVSEFLFGSGFAIAGPLWT 166

RESULT 2

B86819

oxidoreductase ypf [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C;Accession: B86819

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Mallarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ser

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: B86819

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-324 <STO>

A;Cross-references: UNIPROT:Q9SCF7; UNIPARC:UPI00000C6A7B; GB:AE005176; PID:g12724556; P1

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: ypf

A;Gene: BHJ511
C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 40.6%; Score 49.5; DB 2; Length 287;
Best Local Similarity 38.5%; Pred. No. 4.3;
Matches 10; Conservative 4; Mismatches 9; Indels 3; Gaps 1;

Qy 1 LVAEVSEFLFGSGF---AIAEGLPWT 23
| : | : | : | : | : | : | : |
Db 202 LTRSLSESIVGGIRVNGVAPGPIWT 227

RESULT 10
C83824
ABC transporter (permease) BH1395 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83824
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai,
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83824
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <STO>
A;Cross-references: UNIPROT:Q9KD24; UNIPARC:UPI00000D73FO; GB:AF001511; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1395
C;Superfamily: conserved hypothetical protein HI0360

Query Match 40.2%; Score 49; DB 2; Length 287;
Best Local Similarity 40.0%; Pred. No. 5.2;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 4 EVSEFLFGSFAIAGPLWT 23
:: : |||| :: : ||
Db 124 DLWNYLFGSVIAVSRLDWT 143

RESULT 11
D69472
modulation protein NfeD (nfd) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69472
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.L.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69472
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-444 <KLE>
A;Cross-references: UNIPROT:O28493; UNIPARC:UPI0000056BB9; GB:A8000979; GB:AE000782; NID
C;Superfamily: Rhizobium nodulation competitiveness protein nfeD

Query Match 40.2%; Score 49; DB 2; Length 444;
Best Local Similarity 52.6%; Pred. No. 8.4;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 EVSEFLFGSFAIAGPLW 22
||| ||| ||| |||
Db 381 EVLEFSNGRGFARVGEIW 399

RESULT 12
S75398

